US-60-191-637-4899

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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
LOCATION: (73)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
LOCATION: (76)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
LOCATION: (177)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
LOCATION: (177)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids occurring L-amino 
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; Sequence 222, Application PC/TUS0101309
; GENERAL INFORMATION:
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJZ05PCT
CURRENT APPLICATION NUMBER: PCT/US01/01309
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 222
LENGTH: 401
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity 38.1%;
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Best Local Similarity
Matches 9; Conserv
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NAME/KEY: SITE
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LOCATION: (60)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (62)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                 40.8%; Score 48.5;
47.4%; Pred. No. 70;
tive 3; Mismatches
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Search completed: March 27, 2002, 14:20:26 Job time: 1573 sec

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AAW88707

AAW88707

AAG66537

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                                                                                    Glucosyltransferea
L. mesenteroides a
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
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Human interleukin-	AAW48314	19	825		43.5	5
Human interleukin-	AAW60668	19	825		٠	14
Human interleukin-	AAW13499	18	825		w ·	ω
Human IL-4 recepto	AAR11254	12	825			2
Derived amino acid	AAR04575	11	824		ω.	Ξ
IL-13/IL-4 dual tr	220	21	793	37.5	43.5	0
IL-13/IL-4 dual tr	AAY92207	21	784		Ü	39
Human MBSP2 polype	AAB62398	22	739			86
	AAB62397	22	739		Ψ	37
Human secreted pro	AAU00394	22	735			8
	AAY92203	21	694		ω	5
	AAY92201	21	694		$\omega$	34
Fusion polypeptide	AAY92202	21	691		$\omega$	ü
polypep	AAM43563	22	498		ω	ະ
Mature human IL-4R	AAY57326	21	197		ω.	<u>~</u>
-	AAW50026	19	197			ö
Periplasmic chaper	AAR89326	17	259		44.5	9
$\vdash$	AAG92916	22	657		45	8
ein from	AAR32657	14	657		45	27
mays	AAG34332	21	513		45	6
mays protein	AAG44661	21	458		45	Ğ
mays protein	AAG34333	21	458		45	
	AAG44662	21	410			
protein	AAG34334	21	410		45	2
.0	AAG44663	21	409	•	45	1
neumo	AAY35397	20	151		45	õ
	AAG38644	21	560		45.5	9
S. epidermidis ope	AAG81986	22	826	39.7	46	8
	AAG13576	21	460	39.7	46	7
Arabidopsis thalia	38	21	420	39.7	46	9
thal	57	21	412	39.7	46	5
thal	S	21	$\vdash$	39.7	46	4
is tha	313	21	372	39.7	46	ω
Arabidopsis thalia	AAG31391	21	371	39.7	46	5

## ALIGNMENTS

RESULT AAR91047

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Alpha-D-glucosyltransferase; primer-independent; soluble glucan; sucrose; transgenic plant; cloning; Escherichia coli; phage lambda-C13; vector; plasmid pGSG501; plasmid pGSG502; gene transfer; crop improvement; storage carbohydrate; pasture; feedstuff; senescence; dextran; binder; food; pharmaceutical.
WPI; 1996-151376/15
N-PSDB; AAT13139.
                                     Giffard PM,
                                                                                                          24-AUG-1994;
                                                                                                                                  24-AUG-1995;
                                                                                                                                                          29-FEB-1996.
                                                                                                                                                                                                       Streptococcus
                                                                                                                                                                                                                                                                                                                            22-MAY-1996 (first entry)
                                                           (GIFF/) GIFFARD P M.
(JACQ/) JACQUES N A.
(SIMP/) SIMPSON C L.
                                                                                                                                                                                 WO9606173-A1
                                                                                                                                                                                                                                                                                                      Alpha-D-glucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                       AAR91047;
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                                   Jacques
                                                                                                                                                                                                         salivarius strain ATCC 25975
                                                                                                          94AU-0007643
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                                     NA,
                                     Simpson
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Secreted protein e Human interferon-a Arabidopsis thalia Arabidopsis

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RESULT
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Best Local
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The DNA sequence from Streptococcus sobrinus strain 6715 encoc glucosyltransferase-I (and mutants). The DNA was obtd. by tre S. sobrinus 6715 with mutanolysin, extracting the chromosomal partially digesting with Sau3AI and fractionating on agarose 9 The 3-5 kbp fragment was ligated into pUC18 and E. coli JM109 transformed with it. A GT-1 expressing clone was isolated and
                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus
                                                                                                                                                   DNA sequence glucosyl:transferase-I - comprises Streptococcus sobrinus DNA sequence with at least one nucleotide added or
                                                                                                                                                                                                                                                                                                                                                                                 JP05023188-A
                                                                                                                                                                                                                                                                                                                                                                                                                                           GT-1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence represents an alpha-D-glucosyltransferase from Streptococcus sallvarius. The enzyme is primer-independent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 16-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plants contg. new bacterial DNA encoding glucosyl transferase activity - retain higher levels of stored carbohydrate(s) in a readily digestible by ruminants
                                                                                                         Claim 13;
                                                                                                                                                                                                  WPI; 1993-079449/10
N-PSDB; AAQ37760.
                                                                                                                                                                                                                                                                                          25-JUL-1991;
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85.7%;
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Best Local
                                                                                                                                                                                                                           This invention describes a novel nucleic acid molecule (I) encoding alternan sucrase (E.C. 2.4.1.140 - an enzyme, that belongs to the glucosyltransferase group) The recombinant, purified alternan sucrase gene is useful for the fermentative production of alternan (a carbohydrate) and/or fructose by secreting the enzyme into a saccharose-containing culture medium. Alternatively, the enzyme is contacted with a saccharose-containing solution. The alternan and/or
                                                                                                                                                 fructose is then isolated from the medium. Cosmetic products or foodstuffs containing alternan can be produced. Recombinant production alternan sucrase is advantageous as it provides a cost effective means
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      syrup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding recombinant Leuconostoc mesenteroides alternan sucrase protein and methods of alternan and fructose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB10667
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Sequence
                                              producing fructose for high fructose containing syrups, production of which previously has been achieved by costly production from maize starch. This sequence represents the Leuconostoc mesenteroides altern sucrase protein which is described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim la; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    production
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    mesenteroides alternan sucrase protein.

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990S-0123180

990S-0125788

990S-0126785

990S-0128234

990S-0128234

990S-0130449

990S-0130449

990S-0132486

990S-0132486

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promoter;
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RESULT
AAG42076
ID AAG4
XX
AC AAG4
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DT 18-C
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Best Local Similarity 47.8%;
Matches 11; Conservative
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                                         standard;
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990S-0150864
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                                                                                                                  ; Score 50; DB; Pred. No. 10; 3; Mismatches
                                         522
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	99US-0139763. 99US-0139817.	99US-0139463. 99US-0139750.	99US-0139461. 99US-0139462.	99US-0139460.	99US-0139458. 99US-0139459.	99US-0139457.	99US-0139455.	99US-0139454.	99US-0139453.	99US-0139,452.	99US-0138847.	9905-0138540.	990S-0137724.	99US-0137502.	99US-0137222.	99US-0136782.	99US-0136021.	99US-0135629.	99US-0135124.	99US-0134941.	99US-0134370.	99US-0134221.	9905-0134218.	99US-0134256.	99US-0132863.	99US-0132486.	99US-0132484. 99US-0132485.	99US-0132407.	99US-0132048.	99US-0130891.	99US-0130510.	99US-0130077.	990S-0128/14. 990S-0129845.	9908-0128234.	99US-0126785. 99US-0127462	99US-0126264.	990S-0123548. 990S-0125788.	99US-0123180.	00176-0121825	2000EP-0301439.			thaliana.		ication; signal ssay; genetic ma	thaliana protein fragment
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	9US-015106 9US-015108	9US-015088 9US-015106	9US-014993 9US-015056	9US-014990	9US-014972 9US-014992	9US-014972	9US-014917	9US-014936	9US-014856	9US-014834	9US-014817	9US-014793	9US-014741 9US-014741	9US-014730	9US-014719	9US-014730	908-014703	9US-014638 9US-014638	9US-014638	9US-014595 9US-014595	9US-014591	9US-014591	9US-014522 9US-014522	9US-014521	9US-014514 9US-014514	9US-014508	9US-014508	905-014508	9US-014508 9US-014508	9US-014488	9US-014455 9US-014463	9US-014433	9US-014433 9US-014433	9US-014433	9US-014432	9US-014408	9US-014400 9US-014408	9US-014362	9US-014297	9US-014280 9US-014292	9US-014239	9US-014215	9US-014128 9US-014184	9US-014099	99US-0140354. 99US-0140695.	9US-013989 9US-014035

30-AUG-1999; 31-AUG-1999; 01-SEP-1999; 07-SEP-1999;

99US-0151303 99US-0151438

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99US-0151930

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EP1074617-A2
                                                                                  AAB93916 standard;
            Homo sapiens
                          Human; primer;
                                         Human protein
                                                       26-JUN-2001
                                                                     AAB93916;
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                                                                                                                                                        Local
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                                                                                                                     aigmaviisswsenygdpsenkd
                                                                                                                                                 Similarity
11; Conserv
                                                                                                                                                  Conservative
                                                     (first entry)
                                        sequence SEQ ID NO:13888
                                                                                                                                                                            990S-0161359.
990S-0161360.
990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
990S-0162142.
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99US-0161404.
99US-0161405.
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99US-0160770
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99US-0160815
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99US-0159331.
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99US-0156458.
99US-0156596.
                          detection; diagnosis; antisense therapy; gene therapy
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99US-0159584.
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99US-0157753
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                                                                                  Protein; 418
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5-0158232.
5-0158369.
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8-0154039.
8-0154779.
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47.8%;
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Pred. No. 12;
3; Mismatches
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12;
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Human protein 26-JUN-2001 AAB92987;

sequence SEQ

ID NO:11710.

(first entry)

Human; primer; detection; diagnosis; antisense therapy; gene therapy

Homo sapiens

AAB92987

AAB92987 standard; Protein;

531

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                                                                                                                  Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                              of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence, ''-end sequence is selected from those defined in
                                                                                                                                                                                                                                                                       the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ota T,
Ishii 9
                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                     represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; SEQ ID 13888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-318749/34.
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02-MAY-2000;
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27-AUG-1999;
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                                                                                                                                                                                                                                                                      AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
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Sugiyama
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; 2000JP-0183767.
; 2000JP-0241899.
                                                                                                                Conservative
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99JP-0300253
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52.9%;
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EXEXEXEX B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC of an oligonucleotide comprises as sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end CC sequence and an oligonucleotide comprises a gequence complementary to a complementary for a complementary to a complementary to a complementary for the primer sets can be used in antisense therapy and complementary full length cDNAs. The primers are useful for synthesising polynucleotides, complementary full-length cDNAs. The primers are also useful for the complementary full-length cDNAs. The primers allow obtaining of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs complementary full-length cDNAs are complementary to a complementary to the complementary to a complementary to 
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02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 Human; secreted protein; fusion protein; gene therapy; protein therapy;
                                Secreted protein encoded by gene 174 clone HE9FB42
                                                                  01-MAR-1999
                                                                                                                                AAW88707
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                                                                                                                                standard;
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                          Conservative
                                                                 (first entry)
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                                                                                                                                Protein; 623
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A, Nagai K,
                                                                                                                                                                                                                                                                                                     DB 22;
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C, Otsuki
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05-SEP-1997
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06-JUN-1997;
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diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroid; diseation; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

Homo sapiens

W09854963-A2

10-DEC-1998

18-DEC-1997; 98WO-US11422

06-JUN-1997 97US-0048884 97US-0048881 97US-0048877

06-JUN-1997; 97US-0048893

970S 0048896.
970S 00488915
970S 004899.
970S 004899.
970S 0048962.
970S 0049975.
970S 0057658.
970S 0057658.
970S 0057654.
970S 0057664.

97US-0057667.
97US-0057761.
97US-0057770.
97US-0057777.
97US-0057778.
97US-0048875.
97US-0048888.
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97US-0048897.
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97US-0048979.
97US-0048979.

97US-0057642. 97US-0057645. 97US-0057648. 97US-0057651.

970S 0057662 970S 0057668 970S 0057765 970S 0057765 970S 0057771 970S 0057771 970S 0048880 970S 0048880 970S 0048883 970S 0048895 970S 0048895 970S 0048895 970S 0048898

97US-0048963.

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CC encoding human secreted proteins (AAW88534 to AAW88756). The secreted concoding human secreted proteins (AAW88534 to AAW88756). The secreted concoding human sequences are deposited with the ATCC under deposit numbers (CC ATCC 97979, 97974, 97975, 97976, 97977, 209007, 209008, 209009, 209010, (CC 209011, 209080, 209081, 209082, 209083, 209083, 209084, 209085, 209511. Host (CC cells comprising recombinant vectors containing the nucleic acid (CC cells comprising recombinant production of the secreted (CC sequences are used for the recombinant production of the secreted (CC proteins. The polynucleotide and amino acid sequences are useful for are (CC useful for gene therapy, Pathological conditions can be also (CC by protein or gene therapy, Pathological conditions can be also (CC or by determining the amount of the new polynucleotides. (CC or by determining the presence of mutations in the new polynucleotides. (CC or by determining the presence of mutations in the new polynucleotides. (CC or by determining the presence of mutations in the new polynucleotides.) (CC or by determining the presence of mutations in the new polynucleotides. (CC or by determining the presence of mutations in the new polynucleotides. (CC or by determining the presence of mutations in the new polynucleotides.) (CC or by determining the presence of mutations in the new polynucleotides.) (CC or by determining the presence of mutations in the new polynucleotides.) (CC or by determining the presence of mutations in the new polynucleotides.) (CC or by determining the presence of mutations in the new polynucleotides.) (CC or by determining the presence of mutations in the new polynucleotides.) (CC or by determining the presence of mutations in the new polynucleotides.) (CC or by determining the presence of mutations in the new polynucleotides.) (CC or by determining the presence of the new polynucleotides.) (CC or by determining the presence of the new polynucleotides.) 
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06-JUN-1997
05-SEP-1997
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Florence
Li Y, Mo
Shi Y, So
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brewer LA,
                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                            restenosis, prostate diseases, obesity, disorders involving osteoclasts such as osteoporosis, arthritis or malignancies, diseases of testes, lung or thymus, digestive/endocrine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 569-571; 772pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
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e K,
                                                                                  Similarity 52.99; Conservative
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                                                                                                                                                                                                                                      gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carter KC, Dillon PJ, Ebner R, Endre
P, Ferrie AM, Fischer CL, Florence C
Greene JM, Hu J, Kyaw H, Lafleur DW;
PA, Ni J, Olsen HS, Rosen CA, Ruber
t DR, Wei Y, Young P, Yu G, Zeng Z;
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970S-0057654.
970S-0057666.
970S-0057760.
970S-0057763.
970S-0057769.
970S-0057774.
970S-0057777.
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97US-0057627.
97US-0057634.
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97US-0057646.
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97US-0049019.
                                                                                                      42.2%;
52.9%;
                                                                                                                                                                                                                                    represents human secreted protein (see and clone identification).
                                          21
                                                                                Score 49; DB Pred. No. 21; 3; Mismatches
                                                                                                                             20;
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                                                                                                                           Length 623;
                                                                                  Indels
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RESULT

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                                                                                                                  AAG66537
                                                   Matches
                                                              Query Match
Best Local
                                                                                                                                      The invention relates to a method for predicting responsiveness of a patient to treatment with a type I interferon. The method comprises determining the level of one or more proteins with a 646, 164, 126, 59 98, 177, 761, 361, 941, 657, 817, 429, 473, 399, 285 or 303 amino acid sequence fully defined in the specification after treatment with a type I interferon. The method allows a physician to determine whether a patient suffering from chronic viral hepatitis, neoplastic disease or relapsing remitting multiple sclerosis will respond favourably to Type I interferon treatment via oromucosal administration. The present sequence is one of the polypeptides listed above that may be used in the method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; interferon-alpha induced gene; type I interferon treatment; chronic viral hepatitis; relapsing remitting multiple sclerosis; neoplastic disease; SEC 63.
                                                                                                                                                                                                                                                                                              Claim 1;
                                                                                                                                                                                                                                                                                                                     Predicting responsiveness of a patient to treatment with a type I interferon comprising determining the level of induced proteins after treatment with a type I interferon, -
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                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                               Meritet J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-FEB-2000;
11-FEB-2000;
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247 imvlagasefdpgynkd
              5 LSILEAWSDNDPQYNKD
                                                 Similarity
9; Conserv
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2000GB-0003205
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                                                  Conservative
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52
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21-APR 1999
23-APR 1999
23-APR 1999
23-APR 1999
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24-APR 1999
25-MAY 1999
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28-APR 1999
29-APR 1999
21-MAY 1999
21-JUN 1999
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   990S-0123180
990S-0123180
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990S-0128714
990S-0130077
990S-0131490
990S-0132486
990S-0132486
990S-0132486
990S-0132486
990S-0134256
990S-01342768
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990S-0138847
990S-0139453
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mapping; gene expression control;
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promoter;
     30-JUN 1999
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23-JUN-1999;
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28-JUN-1999;
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21-JUN-1999;
9908-0139459
9908-0139461
9908-0139461
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9908-0139773
9908-0140333
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protein fragment

SEQ IJ NO: 37689

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RESULT :
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Best Local S
Matches
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23-SEP-1999;
24-SEP-1999;
28-SEP-1999;
29-SEP-1999;
04-OCT-1999;
05-OCT-1999;
06-OCT-1999;
07-OCT-1999;
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18 · CCT · 1999;
21 · CCT · 1999;
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21 · CCT · 1999;
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27-AUG-1999;
27-AUG-1999;
27-AUG-1999;
27-AUG-1999;
30-AUG-1999;
31-AUG-1999;
01-SEP-1999;
07-SEP-1999;
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16-SEP-1999;
20-SEP-1999;
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13-OCT-1999;
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25 - AUG-
   17-OCT-2000
                                        AAG31391 standard; Protein; 371 AA
                     AAG31391;
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5-OCT-1999;
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  (first entry)
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11-JUN-1999
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990S-0123180
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990S-0126264
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990S-0130410
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990S-0132486
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promoter;
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В δÃ

S-0139817. S-0139899. S-0140353. S-0140354. S-0140695. S-0140823.

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RESULT 13
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ID AAG313
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AC AAG313
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DE Arabid
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KW Protei
KW Protei
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KW termin
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11-SEP-1999
12-SEP-1999
22-SEP-1999
23-SEP-1999
24-SEP-1999
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               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter
                                           Arabidopsis
                                                            17-OCT-2000
                                                                             AAG31390;
                                                                                               AAG31390 standard;
        termination
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166 ilsswtenygdpsenkd
                                                                                                                                                                                             Match
                                                                                                                                                                            Similarity 52.9; Conservative
       sequence
                                          thaliana protein fragment SEQ
                                                            (first
                                                                                                                                                                                                              9908-0151080

9908-0151337

9908-0151930

9908-0153758

9908-0154079

9908-0155569

9908-0155569

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9908-015765

9908-0157865

9908-0158029

9908-015823

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52
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                 promoter;
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99US-0140695.
99US-014091.
99US-014091.
99US-0141287.
99US-0141287.
99US-0142803.
99US-0142803.
99US-0142803.
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99US-014811.
99US-01481.
99US-014972.
99US-014992.
99US-014992.
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99US-014993.
99US-0150866.

21-JUN-1999 22-JUN-1999 23-JUN-1999 24-JUN-1999 28-JUN-1999 28-JUN-1999 29-JUN-1999 01-JUL-1999 01-JUL-1999 01-JUL-1999 11-JUL-1999 11-JU

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11-AUG

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13-AUG-1999 113-AUG-1999 16-AUG-1999 17-AUG-1999 20-AUG-1999 20-AUG-1999 20-AUG-1999 23-AUG-1999 23-AUG-1999 25-AUG-1999 25-AUG-1999 27-AUG-1999 27-AUG-1999

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9US-0149175 9US-0149726 9US-0149726 9US-0149723 9US-0149923 9US-0150884 9US-0151065 9US-0151066 9US-0151066 9US-0151303 9US-0151303 9US-0151303	-0146386 -0146388 -01470389 -01470389 -0147204 -0147302 -0147302 -0147192 -01474103 -01474103 -01474103 -01474103 -01474103 -0148319 -0148319 -0148319	903-01444 903-01444 903-01448 903-01450 903-01450 903-01450 903-01450 903-01450 903-01451 903-01451 903-01452 903-01453	9US-0141 9US-0142 9US-0142 9US-0142 9US-0142 9US-0142 9US-0143 9US-0144 9US-0144 9US-0144 9US-0144

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RESULT 1
AAG13578
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Best Loc
Matches
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28-SEP-1999
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05-OCT-1999
06-OCT-1999
                                                                                         Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence.
 25-FEB-2000; 2000EP-0301439.
                         06-SEP-2000
                                              EP1033405-A2
                                                                    Arabidopsis thaliana
                                                                                                                                      Arabidopsis thaliana
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9908-0155596.
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99US-0154779.
99US-0155139.
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52.9%;
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990S-0139453.
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RESULT 15
AAG13577
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   Query Match
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09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
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                                                                                    06-SEP-2000
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                                                                                                                                                  Protein identification hybridisation assay;
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APPLICANT: NICKOIS, SCOTT E.
TITLE OF INVENTION: Substitutes for Modified Starches and TITLE OF INVENTION: Latexes in Paper Manufacture FILE REFERENCE: 0357CR
CURRENT APPLICATION NUMBER: US/09/210,361
CURRENT FILING DATE: 1998-12-11
EARLIER APPLICATION NUMBER: 09/007,999
EARLIER APPLICATION NUMBER: 08/478,704
EARLIER APPLICATION NUMBER: 08/485,243
EARLIER APPLICATION NUMBER: 08/485,243
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US-09-210-361-6
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Patent No. 6284479
GENERAL INFORMATION:
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Result No.

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EARLIER APPLICATION NUMBER: 09/008,172 EARLIER FILING DATE: 1998-01-16

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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1577 amino acids
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                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: AU PM760
FILING DATE: 24-AUG-1994
TELECOMMUNICATION INFORMATION:
TELEPHONE: 61 2 9957 5944
TELEFAX: 61 2 957 6288
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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APPLICANT: Giffard, Philip Morrison
APPLICANT: Jacques, Nicholas Anthony
TITLE OF INVENTION: Genetic Manipulation of Plants to
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CORRESPONDENCE ADDRESS:
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Pred.
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Pred. No. 8.2e-11
                                Mismatches
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                                               90;
                           1.9e-06;
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                                                            Length 1577;
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; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-09-007-999-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-007-999-2
; Sequence 2, Application US/09007999
; Patent No. 6087559
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                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/210,361
CURRENT FILING DATE: 1998-12-11
EARLIER APPLICATION NUMBER: 09/007,999
EARLIER FILING DATE: 1998-01-16
EARLIER APPLICATION NUMBER: 08/478,704
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 09/009,620
EARLIER APPLICATION NUMBER: 09/009,620
EARLIER APPLICATION NUMBER: 08/485,243
EARLIER APPLICATION NUMBER: 08/485,243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 2
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Best Local Similarity
Matches 15; Conserv
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                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                      SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Nichols, Scott E.
TITLE OF INVENTION: Substitutes for Modified Star
TITLE OF INVENTION: Latexes in Paper Manufacture
FILE REFERENCE: 0356D
CURRENT APPLICATION NUMBER: US/09/007,999
CURRENT FILING DATE: 1998-01-16
EARLIER APPLICATION NUMBER: 08/478,704
EARLIER FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Substitute of INVENTION: Laterial Reference: 0357CR
                                                                                                                                                                                                                                                                                           EARLIER APPLICATION NUMBER: 09/008,172
EARLIER FILING DATE: 1998-01-16
EARLIER APPLICATION NUMBER: 08/482,711
EARLIER FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ
                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                  LENGTH: 1475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
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5. 6284479
                                                              15;
                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scott E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Latexes in Paper Manufacture
                                                                              64.7%;
71.4%;
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71.48;
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Pred. No. 0.00053;
1; Mismatches 5;
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Pred. No. 0.
                                                              Mismatches
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0.00053;
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SOFTWARE: PatentIn Ver. SEQ ID NO 27
LENGTH: 703
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LENGTH: 1375
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Patent No. 6235481
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Best Local :
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CURRENT FILING DATE: 1998-12-11
EARLIER APPLICATION NUMBER: 09/07,999
EARLIER FILING DATE: 1998-01-16
                                                                  CURRENT APPLICATION NUMBER: US/09/422,869 CURRENT FILING DATE: 1999-10-21 EARLIER APPLICATION NUMBER: 60/134,175 EARLIER FILING DATE: 1999-05-13 NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                              APPLICANT: SREENAN, SEAMUS
APPLICANT: ZHOU, YUN-PING
APPLICANT: OTANI, KENICHI
APPLICANT: HANIS, CRAIG L.
APPLICANT: BELL, GRAEG I.
TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
FILE REFERENCE: ARCD:307
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: POLONSKY, KENNETH S. APPLICANT: HORIKAWA, YUKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARLIER APPLICATION NUMBER: 08/485,243
ARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 09/08,172
EARLIER FILING DATE: 1998-01-16
EARLIER APPLICATION NUMBER: 08/482,711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: 08/478,704
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 09/09,620
EARLIER FILING DATE: 1998-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Substitutes for Modified Startitle OF INVENTION: Latexes in Paper Manufacture
                                                                                                                                                                                                                                                                                                                                           APPLICANT: ODA, NAOHISA
APPLICANT: COX, NANCY J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 0357CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09422869
                                                                                                                                                                                                                                                                                                                                           NANCY J.
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66.7%;
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Pred. No. 0.015;
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Best Local Similarity
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US-08-508-761B-31
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US-08-508-761B-31
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                                                                                                                                                                                                                                                                  TELEFAX: (202) 393-531
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Duchiron, APPLICANT: Renaud, MITITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 324 amino acids
                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FR 91/09652
FILING DATE: 29-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91/09870
FILING DATE: 02-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAMM: DISCOT WITHING THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/01 FILING DATE: 31-JUL-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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212 ERWQENDPKSNVD 224
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                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                           NAME: Player, William REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                           9 EAWSDNDPQYNKD 21
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o. 6027920
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                                                                                                                                                                                                                         amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U.S.A.
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                                                          Conservative
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                                                                      38.8%;
53.8%;
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                                                                                                                                                                                                                                                                                                                                           31,409
                                                          Mismatches
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                                                                        Score 45; Pred. No.
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Pred. No. 14;
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RESULT 9 US-08-508-761B-2 ; Sequence 2, Application US/08508761B

Patent No.

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                                                                                                                                                  Sequence 3, Application US/08277231A
Patent No. 5643725
GENERAL INFORMATION:
APPLICANT: Green, Bruce A.
APPLICANT: Brinton, Charles C.
TITLE OF INVENTION: Sequence and Analysis of LKP Pilin
Patent No. 5643725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202) 393-5350 INFORMATION FOR SEQ ID NO:
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APPLICANT:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91
FILING DATE: 29-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 657 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 02-AUG-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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APPLICATION NUMBER:
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                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                  286 ERWQENDPKSNVD
                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: P58525NA
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OPERATING SYSTEM: PC-DOS/MS-DOS
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                               9 EAWSDNDPQYNKD 21
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                                Lexington
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                Massachusetts
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                                                Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          657 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Purification, Relano
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                                                                 Hamilton, Brook,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (202) 638-6666
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53.8%;
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                                                                   Smith & Reynolds, P.C
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Best Local Similarity
Thes 8; Conserve
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Patent No. 5834187 5786143
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/277,321
FILING DATE: 19-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,750
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Structural Gene and the LKP Pili Operon of No. TITLE OF INVENTION: Haemophilus Influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Green, Bruce A.
APPLICANT: Brinton, Jr., Charles C.
TITLE OF INVENTION: Sequence and Analysis of LKP Pilin
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice 0.
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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76 ALVQAWIDNGNPNADPKYTK 95
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                             NAME: Carroll, Alice O. REGISTRATION NUMBER: 33,542
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                 REFERENCE/DOCKET NUMBER:
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GY: linear
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Pred. No. 7.
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               ACC94-02B
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617-861-6240

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                                                Matches
                                                                             Query Match
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APPLICANT: Brinton, Jr., Charles C.
TITLE OF INVENTION: Sequence and Analysis of LKP Pilin
Patent No. 5968769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5968769
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                                                                                                                                                                                                                    TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   equence 6,
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/277 FILING DATE: July 19, 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 259 amino acids
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LENGTH: 259 amino acid
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CORRESPONDENCE ADDRESS:
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les 8; Conserv
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                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 33,542 REFERENCE/DOCKET NUMBER: ACC
                                                                                                                                                                                                                                                                                              NAME: Carroll, Alice O. REGISTRATION NUMBER: 33
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6 SILEAWSDN-----DPQYNK 20 ::::|| || || || || || || ||
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                                                             Score 44.5;
Pred. No. 7
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Pred. No. 7
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US-08-897-020-7
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                                                                                                                                 Sequence 6, Application US/08684024 Patent No. 5834298 GENERAL INFORMATION:
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DESCRIPTION:
                                                                                                       APPLICANT: Benezra, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 33, 91
REFERENCE/DOCKET NUMBER: WH
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: P-91,242
FILING DATE: 19-JUL-1996
ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Bayer Corporation, Pharmaceutical Division STREET: 400 Morgan Lane
                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                        APPLICANT:
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                                                                                          NUMBER OF SEQUENCES:
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SOFTWARE: Word for Windows 6.0
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STATE: CT
                               CITY:
                                           STREET:
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 COUNTRY:
                                                         ADDRESSEE:
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                             New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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New York
                                           1185 Avenue
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linear
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SYSTEM: PC-DOS v. 6.30
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                                                           Cooper &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              812-5492
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High-affinity Interleukin-4 Muteins
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                                           Dunham of the
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                                                                                                       OF MAD2
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RESULT 15
US-09-145-868-6
; MOLECULE TYPE:
JS-09-145-868-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/09145868 Patent No. 6096522
                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION UNMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                         TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2 NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0 FILING DATE: 02-SEP-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Cooper & Dunham LLP STREET: 1185 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                         TOPOLOGY:
                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               RY: U.S.A.
10036
                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
                                                                           205 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Benezra, Robert
                   protein
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                                                                                                                 6.
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160 HLVVPEKWEESGPOF 174

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Matches Query Match

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4; Mismatches Score 42; Pred. No.

5; Indels Length 205;

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Gaps

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DB 2; 15;

; MOLECULE TYPE: protein US-08-684-024-6

TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 205 amino acids
TYPE: amino acid
TOPOLOGY: linear

6:

ATTORNEY AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678

TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400

REFERENCE/DOCKET NUMBER:

1747/46621-A

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/684,024
FILING DATE: 19-UUL-1996
CLASSIFICATION: 435
CLASSIFICATION: 435

ZIP: 10036 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

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                            Query Match
Best Local Similarity
Matches 6; Conserv
4 HLSILEAWSDNDPQY 18
                             Conservative
                                      36.2%;
40.0%;
                            Score 42; DB 3; Pred. No. 15; 4; Mismatches
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                                                  Length 205;
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Search completed: March 27, 2002, 13:59:30 Job time: 583 sec

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Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-290-049-12	US-09-740-274-2	US-09-557-848-2	US-09-290-049-13	US-09-290-049-10	US-09-290-049-1	US-09-740-274-6	US-09-649-885-2	US-09-290-049-11	ID
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US-08-277-231-3	3-681A-	US-09-738-626-6670	US-08-508-761-2	US-08-039-028B-2	-08-039-028A-	US-08-039-028-2	US-09-602-839A-534	312	438-	09 - 198	-09-450	-09-134	242	-09-768	-60-300	-60-296	- 09-	-09-391	-09-391-6	-09-	-09-107-5	,,	-09-107-	-09-595-2	US-09-489-039A-9716	US-09-933-767-422	US-09-205-258-422	PCT-US01-05614-422	-09-9	US-09-205-258-482	-US98-11422A-4	ż	-09-499-203-	US-09-290-049-14 US-09-740-274-4	-00-300-040-
Sequence 3, Appli		e 6670,	'n	ν,	2, Ap	2,	e 534, i	e 8416,	767,	e 815,		3159,	1100	27,	10,	10,		2916	2917	6181	6181	6431		765, i	9716,	422,	e 422,	122, F	e 482,	e 482,	407,	482,	equence 2,	Sequence 14, Appli Sequence 4, Appli	-

## ALIGNMENTS

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APPLICANT: Taubman, Martin A.

APPLICANT: Taubman, Martin A.

TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL

TITLE OF INVENTION: CARIES

FILE REFERENCE: FDC98-01pla

CURRENT APPLICATION NUMBER: US/09/290,049

CURRENT FILINC DATE: 1999-04-12

EARLIER APPLICATION UNMBER: 60/081,550

EARLIER FILING DATE: 1998-04-04

EARLIER FILING DATE: 1998-04-13

EARLIER FILING DATE: 1998-04-13
  B
                                                                                                                                                                         ; TYPE: PRT; ORGANISM: S. US-09-290-049-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-290-049-11
; Sequence 11, Application US/09290049
; GENERAL INFORMATION:
                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 19
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 11
LENGTH: 21
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Matches 21; Conserv
1 AINHLSILEAWSDNDPQYNKD
                    1 AINHLSILEAWSDNDPQYNKD 21
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                                                                         100.0%; Score 116; DB 1 larity 100.0%; Pred. No. 4e-11; Conservative 0; Mismatches
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Sequence 2, Application:

Application US/09649885 DRMATION: Nichols, Scott E.

APPLICANT:

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TYPE: PRT
; ORGANISM: Streptococcus mutans
US-09-649-885-2
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                                                                                                                                                                     ; LENGTH: 1430
TYPE: PRT
; ORGANISM: streptococcus mutans
US-09-740-274-6
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                                                                                                                                                                                                                                                                                                                                                                            PRIOR EILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: 09/007,999
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 08/478,704
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 09/009,620
PRIOR APPLICATION NUMBER: 08/485,243
PRIOR APPLICATION NUMBER: 08/485,243
PRIOR FILING DATE: 1995-06-07
                                                                                                               Query Match
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Best Local !
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SEQ ID NO 2
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PRIOR FILING DATE: 1998-01-16
PRIOR FILING DATE: 08,482,711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/740,274
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 09/210,361
PRIOR FILING DATE: 1998-12-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2000-08-28
PRIOR APPLICATION NUMBER: US 09/008,172
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 08/482,711
PRIOR FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/649,885
CURRENT FILING DATE: 2000-08-28
                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 08/0 PRIOR FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Nichols, Scott E.
TITLE OF INVENTION: Glucan-containing Compositions and Paper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE:
                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID
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495 AINHLSILEAWSDNDPQYNKD 515
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Pred. No. 4.4e-09;
0; Mismatches 0;
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Pred. No. 4.4e-09;
; Mismatches 0;
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APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, Martin A.
APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: SWITHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARIES
FILE REFERENCE: FDC98-01028
CURRENT APPLICATION NUMBER: US/09/290,049
CURRENT FILING DATE: 1999-04-12
EARLIER APPLICATION NUMBER: 60/081,550
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: 60/115,142
EARLIER APPLICATION NUMBER: 60/115,142
В
                                                                                                                                                                            ; ORGANISM: S. mutans US-09-290-049-10
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                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
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                                                                                        Query Match
Best Local Similarity
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                                                                             Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARIES
FILE REFERENCE: FDC98-01.p2A
CURRENT APPLICATION NUMBER: US/09/290,049
CURRENT FILING DATE: 1999-04-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: 60/081,550
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/115,142
EARLIER FILING DATE: 1999-01-08
                                                                                                                                                                                                                   LENGTH: 21
TYPE: PRT
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 21
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1 ANDHLSILEAWSDNDTPYLHD
                                    1 AINHLSILEAWSDNDPQYNKD 21
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                                                                             Conservative
                                                                                              64.78;
71.48;
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71.48;
21
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Pred. No. 0.
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0.00016;
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US-09-290-049-13 ; Sequence 13, Application US/09290049 ; GENERAL INFORMATION:

RESULT

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APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARIES
FILE REFERENCE: FDC98-01p26
CURRENT APPLICATION UNMBER: US/09/290,049
CURRENT FILING DATE: 1999-04-12
EARLIER APPLICATION NUMBER: 60/081,550
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/115,142
EARLIER APPLICATION NUMBER: 60/115,142
EARLIER FILING DATE: 1999-01-08
                                                                                                                                               US-09-740-274-2
; Sequence 2, Application US/09740274
; GENERAL INFORMATION:
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Best Local Similarity
Thes 15; Conserve
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TITLE OF INVENTION: Latexes in Paper Manufacture
FILE REFERENCE: 0356D2
CURRENT APPLICATION NUMBER: US/09/557,848
CURRENT FILING DATE: 2000-04-26
EARLIER APPLICATION NUMBER: 08/478,704
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 09/007,999
EARLIER FILING DATE: 1998-01-16
NUMBER OF SEQ ID NOS: 2
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LENGTH: 21
APPLICANT: Nichols, Scott E.
TITLE OF INVENTION: Glucan containing Compositions and Paper
FILE REFERENCE: 0357cRD
CURRENT APPLICATION NUMBER: US/09/740,274
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 09/210,361
PRIOR FILING DATE: 1998-12-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1475
TYPE: PRT
ORGANISM: Streptococcus mutans
-09-557-848-2
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Local Similarity 75.0%;
es 15; Conservat;
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1 AIDHLSILEAWSGNDNDYVK 20
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71.48;
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Pred. No. 0.00016;
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APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARIES
FILE REFERENCE: FDC98-0102A
CURRENT APPLICATION UNMBER: US/09/290,049
CURRENT FILING DATE: 1999-04-12
EARLIER APPLICATION NUMBER: 60/081,550
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/115,142
EARLIER FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 19
NUMBER OF SEQ ID NOS: 19
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SEQ ID NO 12
LENGTH: 21
TYPE: PRT
ORGANISM: S. downei
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Best Local Similarity
Matches 14; Conserv
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SEQ ID NO 2
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Best Local Similarity 71.4%;
APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARIES
FILE REFERENCE: FDC98-01p2A
CURRENT APPLICATION NUMBER: US/09/290,049
CURRENT FILING DATE: 1999-04-12
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PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 07/008,172
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PRIOR FILING DATE: 195-06-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
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481 ANDHLSILEAWSDNDTPYLHD 50
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Pred. No.
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Pred. No. 0.018;
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0.00023;
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US-09-499-203-2
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US-09-290-049-14
                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: streptococcus mutans US-09-740-274-4
                                                                                                 Sequence 2, Applicat GENERAL INFORMATION:
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                                                                                                                 Sequence
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Best Local
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Best Local Similarity
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                              APPLICANT: WELSH, Thomas APPLICANT: QUANZ, Martin APPLICANT: KNUTH, Karola
TITLE OF INVENT
                                                                              APPLICANT: KOSSMANN, Jens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/740,274
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 09/210,361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Nichols, Scott E.
TITLE OF INVENTION: Glucan-c
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EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/115,142
EARLIER FILING DATE: 1999-01-08
                                                                                                                                                                                                                                                                                                                                                                                            EQ ID NO 4
LENGTH: 1375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/0
PRIOR FILING DATE: 1998-01-20
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PRIOR APPLICATION NUMBER: 09/007,999
PRIOR FILING DATE: 1998-01-16
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                                                                                                                                                                                               507 ANDHLSILEAWSYNDTPYLHD 527
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FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 09/008,172 FILING DATE: 1998-01-16
 OF INVENTION: Nucleic Acid Molecules Encoding Alternansucrase REFERENCE: 147-196P
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                                                                                                               Application US/09499203
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3ER: 09/210,361
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66.7%;
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Pred. No. 0.
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RESULT 14
PCT-US98-11422A-407
PCT-US98-11422A-
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Best Local Similarity
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; LOCATION: (575)
; OTHER INFORMATION: Xaa
PCT-US01-05614-482
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CURRENT FILING DATE: 2000-02-08
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PATENTIN VEr. 2.1
SEQ ID NO 2
LENGTH: 2057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/193,170 PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 1245
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OTHER INFORMATION:
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                   APPLICANT: Human Genome Sciences, Inc., TITLE OF INVENTION: 207 Human Secreted NUMBER OF SEQUENCES: 800
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                                COUNTRY: UZIP: 20850
                                                                                                 STATE: Maryland
                                                                                                                                     CITY: Rockville
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Pred. No.
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Pred. No.
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Query Match
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US-09-205-258-482
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CURRENT FILING DATE: 1998-12-04
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INFORMATION FOR SEQ
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TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
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107 IMVLXGASEFDPQYNKD 123
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TOPOLOGY: linear
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FILING DATE: 04-JUN-1998
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                                                                                                                                                                                                      APPLICATION NUMBER: 60/049,020
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,876
FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/048,880 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,896 FILING DATE: 1997-06-06
                                                                                                                                    FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,884
FILING DATE: 1997-06-06
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                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/049,375
                                                               APPLICATION NUMBER: 60/048,894
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,971
FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/048,885
                                             APPLICATION NUMBER: 60/048,964
                                                                                                                                                                                         APPLICATION NUMBER: 60/048,895
                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1997-06-06
            APPLICATION NUMBER: 60/048,882
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1997-06-06
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52.9%;
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Pred. No.
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US-09-205-258-482
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                             FEATURE:
NAME/KEY: SITE
LOCATION: (575)
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TYPE: PRT
ORGANISM: Homo sapiens
              LOCATION: (575)
OTHER INFORMATION:
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APPLICATION NUMBER: 60/048,898
TTIME DATE: 1997-06-06
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FILING DATE: 1997-66-06
APPLICATION NUMBER: 60/048,875
FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/070,923 FILING DATE: 1997-12-18
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APPLICATION NUMBER: 60/048,897
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Search completed: March 27, 2002, 14:20:25 Job time: 1572 sec

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Sequence 11, Appl
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Sequence 21, Appl
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ALIGNMENTS	US-10-010-802-3	US-09-313-942-32	US-09-611-526-2651	US-09-313-942-30	US-09-313-942-22	US-09-313-942-18	US-09-313-942-20	US-09-614-150-35226	US-09-614-150-423	US-09-708-427-31638	US-09-708-427-31639	US-09-708-427-31640	US-09-708-427-72862	US-09-708-427-72863	US-09-708-427-72864	US-09-620-394B-1365	US-09-708-427-29183	US-09-620-394B-1366	US-09-620-394B-1367	US-09-708-427-29184
	Sequence 3, Appl:	Sequence 32, App.	Sequence 2651, Ap	Sequence 30, Appl	•	Sequence 18, Appl	Sequence 20, App	Sequence 35226, i	Sequence 423, App	Sequence 31638, 1	Sequence 31639,	Sequence 31640,	Sequence 72862, i	Sequence 72863, i	Sequence 72864, A	Sequence 1365, Ap	Sequence 29183, 1	`	Sequence 1367, Ap	Sequence 29184, 1
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## APPLICANT: Smith, Daniel J. APPLICANT: Tabbman, Martin A. TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOI TITLE OF INVENTION: CARIES FILE REFERENCE: 1564.1008-002 CURRENT APPLICATION NUMBER: US/09/290,049A CURRENT FILING DATE: 1999-04-12 PRIOR APPLICATION NUMBER: 60/081,550 PRIOR APPLICATION NUMBER: 60/115,142 PRIOR APPLICATION NUMBER: 60/115,142 PRIOR FILING DATE: 1999-01-08 NUMBER OF SEQ ID NOS: 19 NUMBER OF SEQ ID NOS: 19 SOFTWARE: FastSEQ for Windows Version 4.0 US-09-290-049A-11 ; Sequence 11, Application US/09290049A ; GENERAL INFORMATION: ; ORGANISM: Streptococcus US-09-562-328-22 US-09-562-328-22 GENERAL INFORMATION: APPLICANT: LEES, ANDREW APPLICANT: TAUBMAN, MARTIN A. APPLICANT: SMITH, DANIEL J. APPLICANT: SMITH, DANIEL J. TITLE OF INVENTION: CONJUGATE VACCINES FOR THE PREVENTION OF DENTAL CARIES FILE REFERENCE: 04995.0046-01 NUMBER OF SEQ ID NOS: 44 SOFTWARE: PATENTIN Ver. 2.1 SEQ ID NO 22 LENGTH: 21 Query Match Best Local Similarity CURRENT APPLICATION NUMBER: US/09/562,328 CURRENT FILING DATE: 2000-05-01 LENGTH: 21 TYPE: PRT PRIOR APPLICATION NUMBER: 09/288,965 PRIOR FILING DATE: 1999-04-09 1 AINHLSILEAWSDNDPQYNKD 21 AINHLSILEAWSDNDPQYNKD 21 Application US/09562328 Conservative 100.0%; 0; Score 116; DB 6; Pred. No. 9.3e-12; ; Mismatches 0; FOR DENTAL Length 21; Indels 0 Gaps

; ORGANISM: S. mutans US-09-290-049A-11

SEQ ID NO LENGTH:

TYPE: PRT

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CURRENT APPLICATION NUMBER: US/09/562,3
CURRENT FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 09/288,965
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                    APPLICANT: LEES, ANDREW
APPLICANT: TAUBRAN, MARTIN A.
APPLICANT: SMITH, DANIEL J.
TITLE OF INVENTION: CONJUGATE VACCINES FOR THE PREVENTION OF DENTAL CARIES
FILE REFERENCE: 04995.0046-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/604,957
CURRENT FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 00201871.1
PRIOR FILING DATE: 2000-05-25
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APPLICANT: DIJKHUIZEN, LUBBERT
APPLICANT: RAHAOUI, HAKIM
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RESULT

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Query Match
Best Local Similarity
Watches 15; Conserv:
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SEQ ID NO 24
LENGTH: 21
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                                                                                                                                                                                                                                                      SEQ ID NO 1
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/290,049A
CURRENT FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/115,142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/56: CURRENT FILING DATE: 2000-05-01 PRIOR APPLICATION NUMBER: 09/288,965 PRIOR FILING DATE: 1999-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: TAUBMAN, MARTIN A.
APPLICANT: SMITH, DANIEL J.
TITLE OF INVENTION: CONJUGATE VACCINES FOR THE PREVENTION OF DENTAL CARIES
FILE REFERENCE: 04995.0046-01
                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Smith, Daniel J. APPLICANT: Taubman, Martin
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NUMBER OF SEQ ID NOS: 44
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                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1999-01-08
                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 1564.1008-002
                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                        LENGTH:
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                   1 AINHLSILEAWSDNDPQYNKD 21
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75.0%;
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71.48;
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Pred. No. 2.4e
1; Mismatches
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Pred. No.
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US-09-562-328-23
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LENGTH: 21
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APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, Martin
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Best Local Similarity
Matches 15; Conserv
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TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARLES
FILE REFERENCE: 1564.1008-002
CURRENT APPLICATION NUMBER: US/09/290,049A
CURRENT FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR FILING DATE: 1998-04-13
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CURRENT FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARIES
FILE REFERENCE: 1564.1008-002
APPLICANT: LEES, ANDREW
APPLICANT: TAUBMAN, MARTIN A.
APPLICANT: SMITH, DANIEL J.
TITLE OF INVENTION: CONJUGATE VACCINES FOR THE PREVENTION OF DENTAL CARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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les 15; Conserv
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                                                                                               Application US/09562328
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71.48;
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75.08;
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Pred. No. 2.4e-05;
"""" tches 4;
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Pred. No. 2.
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2.4e-05;
5;
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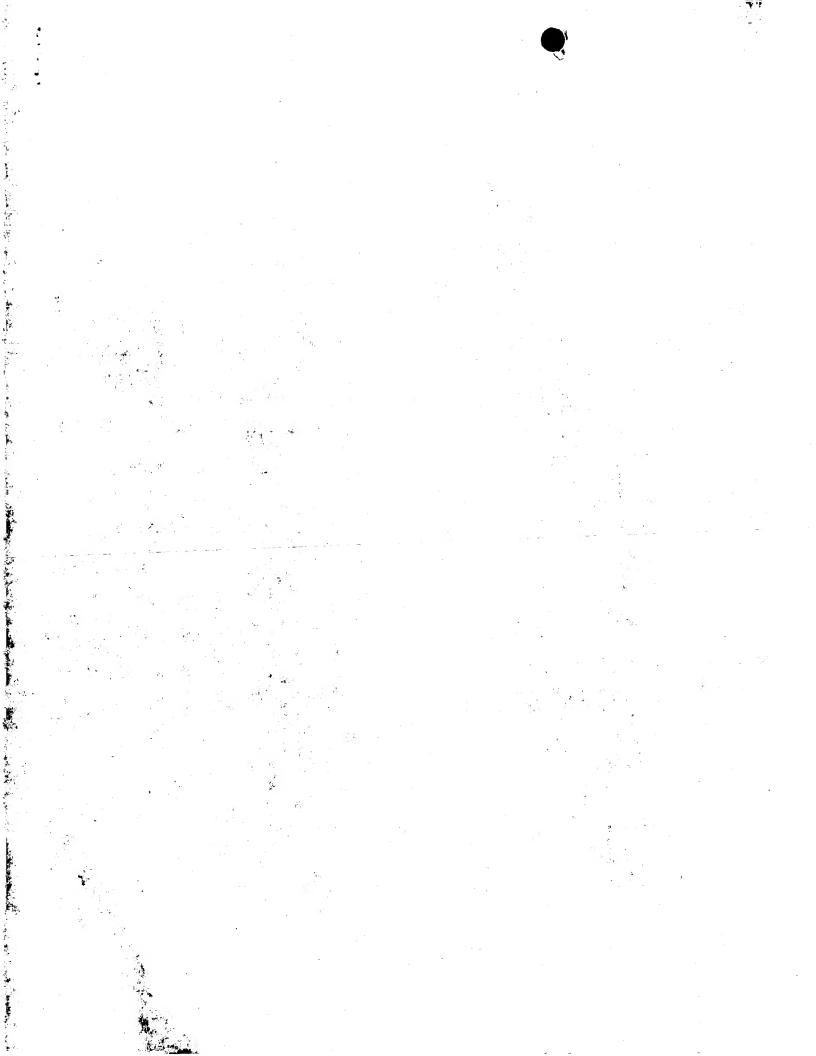
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Sequence 12, Application US/09290049A
GENERAL INFORMATION:
APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: CARIES
FILE REFERENCE: 1564.1008-002
CURRENT APPLICATION NUMBER: US/09/290,049A
CURRENT APPLICATION NUMBER: 60/081,550
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/15,142
PRIOR FILING DATE: 1998-01-08
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 21
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; SEQ ID NO 23
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Streptococcus sp.
US-09-562-328-23
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GENERAL INFORMATION:
APPLICANT: LEES, ANDREW
APPLICANT: TAUBMAN, MARTIN A.
APPLICANT: SMITH, DANIEL J.
TITLE OF INVENTION: CONJUGATE VACCINES FOR THE PREVENTION OF DENTAL CARIES
FILE REFERENCE: 04995.004467.
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Best Local Similarity
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Best Local Similarity
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CURRENT FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 09/288,965
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 44
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CURRENT FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 09/288,965
PRIOR FILING DATE: 1999-04-09
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66.7%;
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Pred. No.
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Pred. No. 3.4e-05,
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                                                                                     ; TYPE: PRT ; ORGANISM: Leuconostoc mesenteroides US-09-604-957-5
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SEQ ID NO 5
LENGTH: 523
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LENGTH: 21
   Matches
                   Query Match
Best Local Similarity
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Best Local Similarity
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APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, Martin A.
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                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/604,957
CURRENT FILING DATE: 2000-06-28
                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASE AND NOVEL GLUCAN FILE REFERENCE: BO 43388
                                                                                                                                                                                                                                                                                                                   APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
APPLICANT: DIJKHUIZEN, LUBBERT
APPLICANT: RAHAOUI, HAKIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARIES
FILE REFERENCE: 1564.1008-002
                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 00201871.1 PRIOR FILING DATE: 2000-05-25
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                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 17
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nes 14; Conservative
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Pred. No. 3.4e-05;
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Score 68; DB 6; Pred. No. 0.012; 0; Mismatches
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Pred. No. 3.
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US-09-562-328-21
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Best Local Similarity
Matches 14; Conserv
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SEQ ID NO 21
LENGTH: 21
TYPE: PRT
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                                                                             Query Match
Best Local Similarity
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APPLICANT: SMITH, DANIEL J.
TITLE OF INVENTION: CONUGATE VACCINES FOR THE PREVENTION OF DENTAL CARIES
FILE REFERENCE: 04995.0046-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/:
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: LEES, ANDREW APPLICANT: TAUBMAN, MARTIN A.
                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 00201871.1 PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/604,957
CURRENT FILING DATE: 2000-06-28
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASE AND NOVEL GLUCAN FILE REFERENCE: BO 43388
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
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TYPE: PRT
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75 ANKHLSILEDWNGKDPQY 92
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Pred. No. 0.00061
                                                                                   Score 64; DB 6;
Pred. No. 0.057;
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Search completed: March Job time: 1694 sec

27, 2002, 14:22:47



GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

OM protein - protein search, using sw model

Run on: March 27, 2002, 14:01:18; Search time 102.51 Seconds

(without alignments)
15.605 Million cell updates/sec

Title: Perfect score: US-09-290-049A-11 116 1 AINHLSILEAWSDND

AINHLSILEAWSDNDPQYNKD 21

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

219241 seqs, 76174552 residues

Searched:

al number of hits satisfying chosen parameters: 219241

Imum DB seq length: 0
.mum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

29	28	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7 7	6	5	4	ω	2	1	Result No.
45	4 4	4.5	45	45	45.5	46	46	46	46	46	47	47	47	47	47	49	66	67	89	74	75	78	81	85	85	90	116	Score
	38.0		•			39.7	39.7	39.7	39.7	39.7	40.5	40.5	40.5	40.5	•	42.2	56.9	•	•	٠	64.7	•	•	73.3		77.6	100.0	Query Match
637	504	344	194	194	250	703	626	623	420	418	491	445	418	403	175	632	1375	1599	1518	1592	1475	1508	1365	1449	1449	1577	1431	Length
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## ALIGNMENTS

X400000x7444446000xxx

В Query Match 100.0%; Score 116; DB 2; Best Local Similarity 100.0%; Pred. No. 1.7e-09; Matches 21; Conservative 0; Mismatches 0; 495 AINHLSILEAWSDNDPQYNKD 515 1 AINHLSILEAWSDNDPQYNKD 21 Length 1431; Indels 0; Gaps

0

glucosyltransferase - Streptococcus salivarius
(;Species: Streptococcus salivarius
C;Species: Streptococcus salivarius
C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 22-Oct-1999
C;Accession: T30858
R;Simpson, C.L.; Giffard, P.M.; Jacques, N.A.
Infect. Immun. 63, 609-621, 1995
A;Title: Streptococcus salivarius ATCC 25975 possesses at least two genes co
A;Reference number: Z20909; MUID:9512Z197
A;Accession: T30858
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1577 <SIM>
A;Residues: 1-1577 <SIM>
A;Cross-references: EMBL:L35928; NID:g662380; PID:g662381; PIDN:AAC41413.1
C;Genetics: at least two genes coding for

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RESULT
T30552
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T30857
glucosyltransferase (EC 2.4.1.-) gtfS precursor -
C; Species: Streptococcus sobrinus
C; Date: 30-Jun-1992 #sequence_revision 30-Jun-199;
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C;Species: Streptococcus salivarius
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999
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C;Species: Streptococcus salivarius
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_ch
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A;Molecule type: DNA
A;Residues: 1-1449 <SIM>
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htted to the EMBL Data Library, February 1998
escription: Streptococcus salivarius V1477 gtf
eference number: Z20854
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18; Conser
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30-Jun-1992 #text_change 15-Oct-1999
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C:Accession: T31098
R:Monchois, V.; Remaud-Simeon, M.; Monsan, P.; Willemot, R.M. FEMS Microbiol. Lett. 159, 307-315, 1998
A:Title: Cloning and sequencing of a gene coding for an extra A:Reference number: Z20981; MUID:98164374
A;Molecule type: DNA
A;Residues: 1-1475 <SHI>
A;Cross-references: GB:M17361; NID:g153639; PIDN:AAA88588.1;
R;Shiroza, T.; Ueda, S.; Kuramitsu, H.K.
submitted to the Protein Sequence Database, September 1990
                                                                                                                         R;Shiroza, T.; Ueda, S.; Kuramitsu, H.K.
J. Bacteriol. 169, 423-4270, 1997
A;Title: Sequence analysis of the gtfB gene
A;Reference number: A33135; MUID:87308013
A;Accession: B33135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Gilmore, K.S.; Russell, R.R.B.; Ferretti, J.J. Infect. Immun. 58, 2452-2458, 1990
A;Title: Analysis of the Streptococcus downei gtfs A;Reference number: A41483; MUID:90316665
A;Accession: A41483
                                                                                                                                                                                                                                  C;Species: Streptococcus mutans
C;Date: 23-Oct-1990 #sequence_revision
C;Accession: B33135; A33128
                                                                                                                                                                                                                                                                                                                                                                                                            Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Description: produces dextran composed only of al C; Keywords: glycosyltransferase; hexosyltransferase
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C;Accession: T31098
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C;Keywords: glycosyltransferase; hexosyltransferase
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A; Residues: 1-1365 <GIL>
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R; Gilmore, K.S.; Ru:
                                                                                                                                                                                                                                                                                                 gtfB protein precursor - Streptococcus mutans
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A;Experimental source
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A; Residues: 1-1508 < MON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable dextransucrase (EC 2.4.1.5), extracellular - Leuconostoc mesenteroldes C; Species: Leuconostoc mesenteroides
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                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Function:
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Best Local S
Matches 15
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Best: Local Similarity
Matches 16; Conserv
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| |||||| || || || 58
63 ANQHLSILEDWSHNDPEYVKD 58
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e: strain NRRL
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71.48;
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76.2%;
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Pred. No.
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Pred. No. 0.00038
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B-1299
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0.0012;
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                                             PID: g153640
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A; Reference number: A38175; MUID:91123227
A; Rocession: A38175
                                                                                                  glucosyltransferase (EC 2.4.1.-) I - Streptococcus salivarius C;Species: Streptococcus salivarius C;Species: Streptococcus salivarius C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 15-Oct-1999 C;Accession: A44811; S22726; S28809 R;Giffard, P.M.; Simpson, C.L.; Milward, C.P.; Jacques, N.A. J. Gen. Microbiol. 137, 2577-2593, 1991 A;Title: Molecular characterization of a cluster of at least two glucosyltransferase gen A;Reference number: A44811; MUID:92148377 A;Accession: A44811; MUID:92148377
A; Molecule type: DNA
A; Residues: 1-1518 <GIF>
A; Residues: 1-1518 <GIF>
A; Cross-references: EMBL: Z11873; NID: 947526; PIDN: CAA77900.1;
A; Cross-reference extracted from NCBI backbone (NCBIN: 81050, NC
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A44811
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C;Species: Streptococcus sobrinus
C;Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 15-Oct-1999
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A; Accession: A33128
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A; Residues: 1-1592 <ABO>
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Pred. No. 0.0054;
2; Mismatches
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                    1; PID:g47527
NCBIP:81052)
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A; Aperimental source: ATCC 25975

R; Giffard, P.M.; Simpson, C.L.; Milward, C.P.; Jacques, J. Gen. Microbiol. 137, 2577-2593, 1991

A; Title: Molecular characterization of a cluster of at A; Reference number: A444811; MUID:92148377

A; Molecular 528810
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A; Molecule type: DNA
A; Residues: 1-51 <GIF>
A; Residues: 1-51 <G
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C:Superfamily: cpl repeat homology
C:Keywords: glycosyltransferase; h
E:1307-1326/Domain: cpl repeat hom
A; Experimental source: GS-5
R; Shiroza, T.; Ueda, S.; Kuramitsu, H.K.
J. Bacteriol. 169, 4263-4270, 1987
A; Title: Sequence analysis of the gtfB gene
A; Reference number: A33135; MUID:87308013
                                                                                                                                                                                                                                                                      Gene 69, 101-109, 1988
A;Title: Sequence analysis of the gtfC gene
A;Reference number: JT0345; MUID:89137980
A;Accession: JT0345
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C;Keywords: glycosyltransferase; hexosyltransferase
F;1456-1475/Domain: cpl repeat homology <CPR>
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A; Residues: 1-1599 <JAC>
A; Cross-references: EMBL:211872; NID:g47530; PIDN:CAA77898.1; PID:g47531
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                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-1375 <UED>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Species: Streptococcus mutans
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Pred. No. 0.04
3; Mismatches
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mology <CP4>

    Streptococcus salivarius

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A;Description: catalyzes the synthesis of both water-soluble and water-insoluble glucans (;Superfamily: cpl repeat homology C;Reywords: duplication; glycosyltransferase; hexosyltransferase F;1-34/Domain: signal sequence #status predicted <SIG> F;35-1375/Product: glucosytransferase #status predicted <MAT> F;1126-1145/Domain: cpl repeat homology <CP1> F;1253-1272/Domain: cpl repeat homology <CP2> F;1318-1337/Domain: cpl repeat homology <CP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein DKFZp434M179.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change (
C;Accession: T46504
R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann,
submitted to the protein Sequence Database, January 2000
                  A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; Mu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                              hypothetical protein (imported) - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: C86205
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-349 <SHI>
                                                                                                                                                                                           R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
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A;Residues: 1-632 <AAA>
A;Croos-references: EMBL:AL137338
A;Experimental source: adult test:
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A; Accession: T46504
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C;Function:
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C;Genetics:
A; Accession: C86205
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                                                                                             Shinn, P.; Southwick, A.M.; Sun,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DВ
13;
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                                                                                                                                               Khaykin,
Maiti, R.
                                                                                                                                               n, E.; Kim,
R.; Marzia
                                                                                                                                                                                                                                                  O.; Alonso; Dewar, K.
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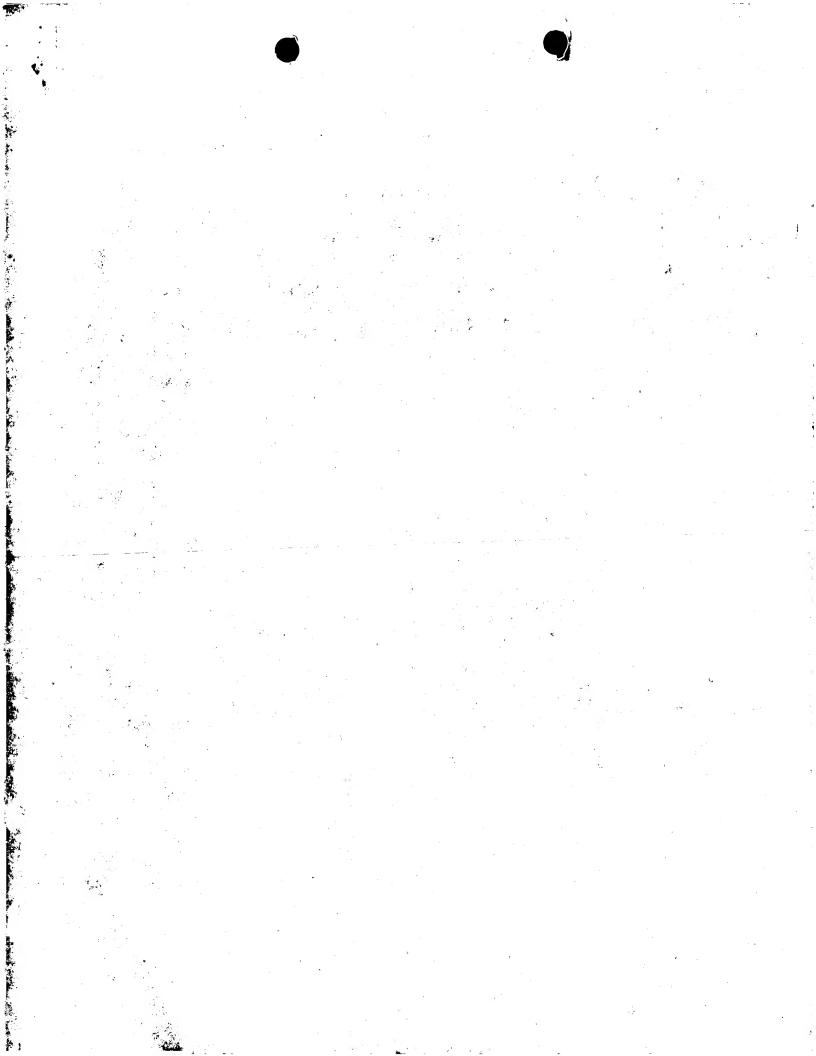
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C;Date: 31-Mar-1989 #sequence_revision 30-Jun-1993 #text_change 16-Jul-1999 C;Accession: A41306; A29708 R;Dermody, T.S.; Schiff, L.A.; Nibert, M.L.; Coombs, K.M.; Fields, B.N. J. Virol. 65, 5721-5731, 1991 A;Title: The S2 gene nucleotide sequences of prototype strains of the three A;Reference number: A41306; MUID:92015462 A;Accession: A41306
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A;Reference number: A29708; MUID:88024195 A;Accession: A29708
                                                                                                                                                                                                                                                                                                                                                                                                   sigma 2 protein - reovirus type
N;Alternate names: core protein
C;Species: reovirus type 1
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A; Authors: Sgares, R.; Sulston, J.E.; Taylor, K.;
A; Taylor: Spares, Biology of Mycobacterium
A; Reference number: A70500; MUID:98295987
A; Accession: B70961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Horris, S.; Seeger, K.; Skelton, S.; Squares, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
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A; Residues: 1-175 <STO>
                                                                                                                                                           A; Molecule type: genomic RNA
A; Residues: 1-418 <DER>
                                                                                                                                                                                                                                                                                                                                                                             A; Note: host Homo sapiens (man)
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A;Experimental source: strain H37Rv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable esterase - Mycobacterium tuberculosis (strain H37RV)
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                                                                                                                R;George,
                                                                                                                                     A; Cross-references: GB:S59098
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                                                                 C.X.; Crowe, A.; Munemitsu, S.M.; Atwater, J.A.; Biophys. Res. Commun. 147, 1153-1161, 1987
Biosynthesis of reovirus-specified polypeptides. P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
9; Conserv
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    reovirus type 1 (strain Lang)

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A;Residues: 1-88,'V',90-204,'Y',206-322,'VATSCMVSKCDEW' <GEO>
A;Cross-references: GB:M17598; NID:g333748; PIDN:AAA47278.1; PID:g333749
C;Genetics:
A;Map position: segment S2
C;Superfamily: reovirus sigma 2 protein
C;Keywords: core protein

Query Match
Guery Match
Best Local Similarity 61.5%; Score 47; DB 1; Length 418;
Best Local Similarity 61.5%; Pred. No. 17;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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Result
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Maximum Match 100%
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Perfect score:
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2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*
4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5: /SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT:*
6: /SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
7: /SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
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Copyright (c) 1993 - 2000 Comp
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AAB36552
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AAY67414
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AAG09941
AAR65965
  AAY60021
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7.834 Million cell updates/sec
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             Glucosyltransferea
Alpha-D-glucosyltr
L. mesenteroides a
Lawsonia intracell
Arabidopsis thalia
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Arabidopsis aldehy
Arabidopsis thalia
T. niveum GAPDH.
                                                                                                                                                                                                                                                          Description
endometrium
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ARESULARA AND AREA AN

Claim 13;

Page 15;

29pp; Japanese

deleted

DNA sequence glucosyl:transferase-I - comprises Streptococcus sobrines DNA sequence with at least one nucleotide added or

WPI; 1993-079449/10. N-PSDB; AAQ37760.

(KATO/) KATO K.

25-JUL-1991 (FUKU/) FUK	25-JUL-199	02-FEB-1993	JP05023188-	Streptococcus	GT-1; Stre	Glucosyltran	28-JUN-199	AAR32925;	JLT 1 32925 AAR32925 s		5 4	. 3	2 4	0 4	9 8	7 4	6 42.	4 4	. 4	30 43	98	7 4	N 10	4 ω	2 4	0	9 4	7 4	16 44	л. <u>4</u>	.ω 	2
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·											Periplasmic chaper Helicobacter polyp	om cl	Arabidopsis thalia Expressed antiqen	abidopsis thali	Arabidopsis thalia Human Fc gamma rec	Corynebacterium gl		Human PTPL1 phosph Amino acid sequenc	Intracellular prot	T. thermophilus nit	Breast cancer asso	Human G3PDH fragme	Arabidopsis thalia	Arabidopsis thalia Arabidopsis thalia	Arabidopsis thalia	C. minitans novel	nic.		J.	Amino acid sequenc	eumoniae pro	glutamicum prot

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Best Local S
Matches 18
                                                  The sequence represents an alpha-D-glucosyltransferase from Streptococcus salivarius. The enzyme is primer independent, and produces soluble glucan from sucrose. A gene encoding the enzyme may be cloned and expressed in Escherichia coll using a subclone of phage lambda-Cl3, e.g. plasmid pGSG501 or plasmid pGSG502. The DNA may also be expressed in a transgenic plant, to improve the level of stored carbohydrate in a pasture plant which normally contains low levels, or to prevent degradation of stored carbohydrae.
                      during
use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sucrose; transgenic plant; cloning; Escherichia coli; phage lambda-Cl3; vector; plasmid p6SG501; plasmid p6SG502; gene transfer; crop improvement; storage carbohydrate; pasture; feedstuff; senescence; dextran; binder: feedstuff;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The DNA sequence from Streptococcus sobrinus strain 6715 encodes glucosyltransferasė-I (and mutants). The DNA was obtd. by treating S. sobrinus 6715 with mutanolysin, extracting the chromosomal DNA, partially digesting with Sau3AI and fractionating on agarose gel. The 3-5 kbp fragment was ligated into pUC18 and E. coli JM109 transformed with it. A GT-1 expressing clone was isolated and sequenced. The clone may be used in the development of a drug for
                                                                                                                                                                                                 Claim 4; Page 16-20;
                                                                                                                                                                                                                                          Plants contg. new bacterial DNA encoding glucosyl transferase activity - retain higher levels of stored carbohydrate(s) in
                                                                                                                                                                                                                                                                                                                                            Giffard
                                                                                                                                                                                                                                readily
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                                                                                                                                                                                                                                                                                                             WPI; 1996-151376/15
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(JACQ/) JACQUES N A.
(SIMP/) SIMPSON C L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09606173-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                       94AU-0007643
                                                                                                                                                                                                                            higher levels
by ruminants
    or to prevent degradation of stored carbohydrate nce. Dextran may be isolated from the plant, for or pharmaceutical additive. Primer independence yme will be functional in plants. The glucan is
                                                                                                                                                                                                                                                                                                                                            NA,
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                                                                                                                                                                                                                                                                                                                                            Simpson CL;
                                                                                                                                                                                                 English.
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Best Local
                                  fructose is then isolated from the medium. Cosmetic products or foodstuffs containing alternan can be produced. Recombinant production alternan sucrase is advantageous as it provides a cost effective means producing fructose for high fructose containing syrups, production of which previously has been achieved by costly production from maize starch. This sequence represents the Leuconostoc mesenteroides alternar
                                                                                                         This invention describes a novel nucleic acid molecule (I) encoding a alternan sucrase (E.C. 2.4.1.140 - an enzyme, that belongs to the glucosyltransferase group) The recombinant, purified alternan sucrase gene is useful for the fermentative production of alternan (a carbohydrate) and/or fructose by secreting the enzyme into a saccharose-containing culture medium. Alternatively, the enzyme is contacted with a saccharose-containing solution. The alternan and/or
                                                                                                                                                                                                                                                                                                                                               (PLAN-)
                                                                                                                                                                                                                                              New nucleic acid encoding alternan sucrase protein a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     poorly degraded in plants but easily degraded by bacteria in the rumen of grazing livestock.
Sequence
                                                                                                                                                                                                           Claim la;
                                                                                                                                                                                                                                     production
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                                                                                                                                                                                                            Page 30-36; 64pp; German.
2057
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                        which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glucosyltransferase; fructose;
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72.28;
                        represents the is described
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                                                                                                                                                                                                                                               g recombinant Leuconostoc mesenteroides and methods of alternan and fructose
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Query Match Best Local S Matches 11

Similarity

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Score 60; DB Pred. No. 2.8; 3; Mismatches

DB 2.8;

Length 2057;

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                                                                                                                                                    The present sequence is the Lawsonia intracellularis flagellar hook
C protein FigE. The present invention describes an isolated or recombinant
C polypeptide (I) that comprises, minics or cross-reacts with a B- or
T-cell epitope of a FigE (flagellar hook) polypeptide from a
Lawsonia spp. (I) has antibacterial activity, and induces a specific
humoral immune response. (I) are used as antigens in vaccines to prevent
or treat infection by Lawsonia, in birds and animals, especially pigs,
C to raise specific antibodies (Ab) and to detect past or present
infection. Ab are also useful in diagnosis, to detect L. intracellularis
or immunologically cross-reactive species, also for identification of
epitopes in FigE. Vectors that contain nucleic acids (II) encoding (I)
as primers or probes for detecting L. intracellularis or related
microorganisms, in hybridisation or amplification assays.
                                                         Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PFIZ )
(AGRI-)
(PIGR-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                             Claim 13; Page 87-90;
                                                                                                                                                                                                                                                                                                                                                                                                                     New immunogenic Lawsonia FlgE peptide, its nucleic acid and antibody, useful in vaccines and diagnosis of Lawsonia infections, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Panaccio M,
Ankenbauer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB36552 standard;
                                                                                                                               Sequence
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AGRIC VICTORIA SERVICES PTY LTD.
PIG RES & DEV CORP.
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                                                         Conservative
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quence.  aliana.  aliana.  pus-0121825 pyus-0121826 pyus-012548 pyus-012548 pyus-0125786 pyus-0126785 pyus-0126785 pyus-0126785 pyus-0126785 pyus-0126786 pyus-0130610 pyus-0130610 pyus-0130610 pyus-0130610 pyus-0130610 pyus-0130610 pyus-0130840 pyus-013486	thaliana protein fragment SEQ ID NO: 7934. tiffication; signal transduction pathway; metabolic pathway;
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RESULT
AAM4 3544
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25-SEP-1999
26-OCT-1999
11-OCT-1999
 Human; antiarthritic; antirheumatic; antiproliferative; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic; neuroprotective; antiallergic; hepatotropic; antidiabetic;
                                                                  Human
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antiparasitic; cardiant; gene therapy; cancer; immune disorder;
cardiovascular disorder; neurological disease; infection; human.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      printed
from WIP
                                                                                                                                              Arabidopsis sp.
                                                                                                                                                                               acetyl CoA
                                                                                                                                                                                                        Arabidopsis; plant plastid; acetyl CoA synthetase; E3 subunit; ACS; plant plastidic pyruvate dehydrogenase; pPDH; ATP citrate lyase; ACL; pyruvate decarboxylase; PDC; aldehyde dehydrogenase; ALDH; acetyl CoA
                                                                                                                                                                                                                                                                                                                                                           AAY67414 stendard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, funga and parasitic infections.
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05-JAN-2001; 2001US-0259678.
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47.4%;
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Pred. No. 24;
3; Mismatches
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      25-FEB-1999;
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09-MAR-1999;
23-MAR-1999;
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Johnson
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N-PSDB; AAZ56975.
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04-MAY-1993;
17-MAY-1993;
New nucleic acid encoding eukaryotic alanine racemase related vectors, host cells and recombinant enzyme, usef producing cyclosporin derivs. or increasing cyclosporin
                                                                              WPI;
                                                                                                                   Kocher
Weber G
                                                                                                                                                                        (SANO
(SANO
                                                                                                                                                                                                                                                                                                                                                                                                                                        Tolypocladium niveum ATCC 34921.
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                                                                                                                                                                        SANDOZ LTD.
SANDOZ PATENT GMBH.
SANDOZ-ERFINDUNGEN VERW GES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                   Schneider-scherzer E,
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
   enzyme, useful for cyclosporin prodn.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 195;
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                This invention describes novel human nucleic acid (cDNA) sequences (A), that are highly expressed in uterine tumour tissue and which have anticancer and cytostatic activity. (A) are used (1) for recombinant expression of polypeptides (B) and (ii) to isolate complete genes. (B) are used (i) to identify agents suitable for treatment of uterine or endometrial cancer; (ii) directly for treating these forms of cancer (including expression from gene therapy vectors) and (iii) for generation of specific antibodies. (A) are identified by assembling ESTs
                                                                                                                                                                                                                                   New nucleic acid sequences expressed in uterine cancer tissues, derived polypeptides, for treatment of uterine and endometrial cand identification of therapeutic agents
                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                       N-PSDB; AAZ42007.
                                                                                                                                                                                                                                                                                                                                                                              Rosenthal A,
                                                                                                                                                                                                                                                                                                                                                                                                                     (META-) METAGEN GES GENOMFORSCHUNG MBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treatment;
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8; Conservative
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                                                                                                                                                                                                  Page 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uterine;
sequence
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  tags) from a particular tissue type before comparison
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                                                                                                                                                                                                                                                                                                                                                                            Hinzmann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer; anticancer;
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07-APR-2000;
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                                                                                                                                 analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the particularly constitution of the control of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organic
                                                                                                                                                                                                                                                                                                                           sequences from the Coryneform bacterium Corynebacterium are useful for identifying the mutation point of a gene mutant of coryneform bacterium, measuring expression amountaint of coryneform bacterium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nakagawa S,
Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coryneform bacterium;
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                                     Note: The sequence data for this patent did not form specification, but was obtained in electronic format
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-DEC-2000;
                                                                                                           in the exemplification of the invention.
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nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO: 4571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118
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2000JP-0159162.
2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mizoguchi H,
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da M,
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Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ochiai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 118;
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                                                                                                                                                                                                                                                                                                                                                                                                     glutamicum.
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Best Local
                                                                Query Match
Best Local
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                                                   Matches
                                                                                                                                                              AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAY91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions.
                                                                                                                                                                                                                                                                                                                                                                                 Griffais
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C. pneumoniae protein involved
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                                                                                                                                                                                                                                                                                                                           Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-357842/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9927105-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY35244;
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                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                 Page 1086-1087; Disclosure; 1912pp; English.
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21-NOV-1997;
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ndrffklvawydnetgy 320
                                                9; Conserv
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                                                                                                                                          where the vector directs the expression of a neutralising {\tt C.} pneumoniae.
                                                                                                                 336 AA;
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                                                   Conservative
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97FR-0014673
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41.2%;
                                                               38.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            epitope
                                                Score 46; DB Pred. No. 46; 1; Mismatches
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Pred. No.
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25;
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                                                                         Length 336;
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                                                  Indels
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RESULT

cellulose; carbohydrate binding domain; CBD; fungi; cellulase.

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                                                                                                                          RESULT 15
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                                                                                                                                                                                                                                                                                                             The specification describes the use of p53 transcription tags for developing products to determine p53 status, to diagnose cancer and to evaluate cytotoxicity or carcinogenicity of a test agent.

A method for diagnosing cancer or determining p53 status in a sample suspected for being neoplastic comprises comparing the level of transcription of an RNA transcription of the transcript in a second sample (s1) of a second tissue (s2), where s1 is suspected of being neoplastic and s2 is a normal human tissue (of the same type) and the transcript is identified by a tag; and categorizing s1 as neoplastic or as having a mutant p53 when transcription is found to be the same cor lower in the first, than in s2. The methods and products can be used to determine p53 status, to diagnose cancer and to evaluate cytotoxicity or carcinogenicity of a test agent. AAY23992-Y24000 represent human PIG
                                                                                                                                                                                                             Query Match
Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of
cancer
                      Fusarium oxysporum F-family cellobiohydrolase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of a human PIG protein
                                               11-FEB-1992
                                                                         AAR15238;
                                                                                              AAR15238 standard; Protein;
                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                     proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-443793/37
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17-SEP-1997;
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                                                                                                                                                                                                              l Similarity
11; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p53\ \text{transcription} tags to determine p53\ \text{status} in, diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UNIV JOHNS HOPKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 67;
                                                                                                                                                                                                                                                                              236
                                                                                                                                                                                                                Conservative
                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polyak K,
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97US-0059153.
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                                                                                                                                                                                                                         37.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     p53 status; cancer; cytotoxicity; carcinogenicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vogelstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                 385
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                                                                                                                                                                                                             Score 45; DB Pred. No. 44; 3; Mismatches
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                                                                                                                                                                                                                                      Length 236;
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Search completed: March 27, 2002, 13:57:55 Job time: 523 sec
                                                                                                                                                                                                    Query Match 37.8%;
Best Local Similarity 24.4%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                          The full-length F-family cellobiohydrolase coding sequence was isolated from a F.oxysporum cDNA library by hybridisation to PCR generated genomic oligonucleotide probes (see esp. AAQ15504). The enzyme encoded by the sequence has a CBD which is homologous to a terminal A region of T.reesei cellulase and is able to bind to insoluble (hemi)cellulosic substrates. See AAQ14838-Q14842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Domain
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                                                                                                                                                                                                                                                                                                                    Sequence
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N-PSDB; AAQ14839.
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RESULT 1 US-09-007-999-2 Sequence 2, Applica Patent No. 6087559 GENERAL INFORMATION APPLICANT: Nichols TITLE OF INVENTION		45	44	43										33	32	31	30	29	28	
999-2 2, Apj 0. 608 INFORM INT: N1:		39	39	39	39.5	39.5	39.5	39.5	39.5	39.5	39.5	39.5	39.5	39.5	40	40	40	40	40	
9-2 , Application US/09007999 , 608752 FORWATION: : Nichols, Scott E. : INVENTION: SUBSTITUTES for TAURITY STATES IN PAGE TOWERTION INTERCES IN PAGE TOWERTHER TOWER		2	2	2	ω	ω.	ω.	ω.	ω	ω	ω.	ω.	ω.	33.2	ω.	ω.	ω.	ω.	ω.	
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and		2,	2	2	4	4	4,	4	4	4,	4,	Sequence 4, Appli	Patent No. 5171684	٠.	2,		œ	4,	Sequence 2, Appli	

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GENERAL INFORMATION:
APPLICANT: NICHOLS, Scott E.
TITLE OF INVENTION: Substitutes for modified Starches and
TITLE OF INVENTION: Latexes in Paper Manufacture
FILE REFERENCE: 0357CR
CURRENT APPLICATION NUMBER: US/09/210,361
CURRENT FILING DATE: 1998-12-11
EARLIER APPLICATION NUMBER: 09/007,999
EARLIER APPLICATION NUMBER: 09/07,999
EARLIER FILING DATE: 1998-01-16
EARLIER FILING DATE: 1998-01-07
EARLIER FILING DATE: 1998-01-09/09,620
EARLIER FILING DATE: 1998-01-20
EARLIER FILING DATE: 1998-01-20
EARLIER APPLICATION NUMBER: 08/485,243
EARLIER FILING DATE: 1998-01-09
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; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-09-007-999-2
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US-09-210-361-2
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                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Applicat Patent No. 6284479 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/007,999
CURRENT FILING DATE: 1998-01-16
EARLIER APPLICATION NUMBER: 08/478,704
EARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 2
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Latexes in Paper Manufacture FILE REFERENCE: 0356D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 481 ANDHLSILEAWSDNDTPYLHD 501
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                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09210361
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LENGTH: 1475
: TYPE: PRT
: ORGANISM: Streptococcus mutans
US-09-210-361-2
                                                                                                                                                                       US-09-008-172-2
                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER APPLICATION NUMBER: 08/485,243
EARLIER FILING DATE: 1995-06-07
EARLIER FILING DATE: 1998-01-16
EARLIER FILING DATE: 1998-01-16
EARLIER APPLICATION NUMBER: 08/482,711
EARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 1375
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Best Local Sim
Matches 21;
                                                                                 Sequence 2, Application US/09008172
Patent No. 6127602
GENERAL INFORMATION:
APPLICANT: Nichols, Scott E.
                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity
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                      TITLE OF INVENTION: Substitutes for Modified Starch TITLE OF INVENTION: Latexes in Paper Manufacture FILE REFERENCE: 0358D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 0357CR
CURRENT APPLICATION NUMBER: US/09/210,361
CURRENT FILING DATE: 1998-12-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Substitutes for modified statement of invention: Latexes in Paper Manufacture
CURRENT APPLICATION NUMBER: US/09/008,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: 09/007,999
EARLIER FILING DATE: 1998-01-16
EARLIER APPLICATION NUMBER: 08/478,704
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 09/009,620
EARLIER FILING DATE: 1998-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER APPLICATION NUMBER: 08/482,711 EARLIER FILING DATE: 1995-06-07 NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER APPLICATION NUMBER: 09/008,172 EARLIER FILING DATE: 1998-01-16
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95.2%;
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Pred. No. 1.7e-09;
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; TYPE: PRT ; ORGANISM: Streptococcus mutans US-09-008-172-2
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             GENERAL INFORMATION:
APPLICANT: Simpson, of APPLICANT: Giffard, if APPLICANT: Jacques, of TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                         Sequence 2, Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1430
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Patent No. 6284479
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Best Local Similarity
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CURRENT FILING DATE: 1998-12-11
EARLIER APPLICATION NUMBER: 09/007,999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 09/008,172
EARLIER FILING DATE: 1998-01-16
EARLIER APPLICATION NUMBER: 08/482,711
EARLIER FILING DATE: 1995-06-07
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NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
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EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 09/009,620
EARLIER FILING DATE: 1998-01-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Nichols,
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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                                                                                                                         , Application US/08793824 5981838
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Substitutes for Modified Starches
                                                                                                                                                                                                                                                                                                                        63.0%;
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Increase
2
                               Nicholas Anthony
Genetic Manipulation of Plants
                                                                   Christine Lynn
Philip Morrison
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                                                                                                                                                                                                                                                                                                                       Score 75; DB 4;
Pred. No. 0.00084;
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Pred. No.
                Stored
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                Carbohydrates
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NUMBER OF SEQUENCES

0;

CORRESPONDENCE ADDRESS:

ADDRESSEE:

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Query Match
Best Local Similarity
Watches 13; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 us-08-361-920-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: AU PM76.
FILING DATE: 24-AUG-1994
TELECOMMUNICATION INFORMATION:
TELEPHONE: 61 2 9957 5944
TELEFAX: 61 2 957 6288
                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 54570460 No. 5457046disk of No.
                                                                                                                                                                                                                                                                                                APPLICANT: Hagen, Frederick
APPLICANT: Hjort, Carsten M.
APPLICANT: Sven, Hastrup
TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
TITLE OF INVENTION: or Hemicellulose
NUMBER OF SEQUENCES: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
ORIGINAL SOURCE:
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LENGTH: 1577 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Woeldike, Helle F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      591 HLSILEAWSYNDHQYNKD 608
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TELEFAX: 01
                                                                                                                                                                             COUNTRY: United ZIP: 10174-6201
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                                                                                                                                                                                                                               CITY: New York
                                                                                                                                                                                                                                                  STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
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                                   FILING DATE:
                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 HLSILEAWSDNDTPYLHD 21
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: United States of America
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o. 5981838th Sydney
                                                                                                                                                                                                                                                405 Lexington Avenue, 62nd Floor
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                                                  US/08/361,920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 34
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/361,920
FILING DATE: 22-DEC-1994
APPLICATION NUMBER: US 07/940,860
APPLICATION NUMBER: 28-CCT-1992
APPLICATION NUMBER: 28-CCT-1992
APPLICATION NUMBER: 28-CCT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose TITLE OF INVENTION: or Hemicellulose NUMBER OF SEQUENCES: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 08-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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                                                               FILING DATE: 28-OCCAPPLICATION NUMBER: FILING DATE: 09-MA
                                                                                                                                                                                 APPLICATION NUMBER: US/08/479,939 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 212-867-0298
                                                                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                   COUNTRY: United
ZIP: 10174-6201
                                                                                                                                                                                                                                                                                                                                                                   STATE: New York
                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
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5686593
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: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                  405 Lexington Avenue,
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Hjort, Carsten M.
Sven, Hastrup
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                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                    No. 56865930 No. 5686593disk of No. 5686593th America, Inc
                                                                   09-MAY-1990
                                                                                                                                                                                                                                                                                                  Floppy disk
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                    08-MAY-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helle F
                                                                                  DK 1158/90
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                                    PCT/DK91/00124
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Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                  62nd Floor
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US-08-483-432-23

; Sequence 23, Appli

; Patent No. 5763254
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Best Local Similarity
                                                    TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 212-867-0298 INFORMATION FOR SEQ ID NO:
                                                                                                           REFERENCE/DOCKET NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3435.204-US
TELECOMUNICATION.INFORMATION:
TELEPHONE: 212-807-0123
TELEPAX: 212-867-022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/940,860
FILING DATE: 28-CCT-1992
APPLICATION NUMBER: DK 1158/90
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK91/00124
                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/361,920
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose TITLE OF INVENTION: or Hemicellulose NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
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LENGTH: 385 amino acid
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MOLECULE TYPE:
                                                                                                                                                                                                                                FILING DATE: 08-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hagen, Frederick
APPLICANT: Hjort, Carsten M.
APPLICANT: Sven, Hastrup
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TELEFAX: 212-867-0298
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                                                                                             TELEPHONE: Z12 CONTROL TO NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/OFFILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                  TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
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10174-6201
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405 Lexington Avenue, 62nd Floor
                                                    385 amino acids
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Pred. No. 13;
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 384
TYPE: PRT
ORGANISM: Coniothyrium minitans
US-09-311-170-2
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Best Local Similarity
Thes 9; Conserva
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Patent No. 6121034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Patent No.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Laroche et al., Andre L. TITLE OF INVENTION: Xylanase cxyl FILE REFERENCE: xylanase cxyl CURRENT APPLICATION NUMBER: US/09/311,170 CURRENT FILING DATE: 1999-05-13 NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/596,291
FILING DATE: 09-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/115,573
                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                             APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: HELDIN, CARL-HERRIK
TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCE
TITLE OF INVENTION: TYROSINE PHOSPHATASES
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328 ANDYLTVMNGCLAVPKCVGITVWGVSDKDSWRSSDSPLLFD 368
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                                                                                                                                                                                                                                                              CITY: BOSTON
                                                                                                                                                                                                                         COUNTRY:
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5821075
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SARAS, JAN
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Pred. No. 19;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
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Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Length 384;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 385
                                                                                                                                                                                                                                                                                                                                                                     FOR NOVEL PROTEIN
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REGISTRATION NUMBER: 31 REFERENCE/DOCKET NUMBER:

EDWARD R.

31,616

LO461/7000

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US-09-100-804-3
; Sequence 3, Application US/09100804
; Patent No. 6066472
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Matches 9; Conserv
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APPLICANT: GONEX, LEONEL JORGE

APPLICANT: SARAS, JAN

APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: HELDIN, CARL-HENRIK

TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL

TITLE OF INVENTION: TYROSINE PHOSPHATASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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TELEX: 92-1742 EZEKIEL
INFORMATION FOR SEQ ID NO: 3:
                                      INFORMATION FOR SEQ ID NO:
                                                                                         REFERENCE/DOCKET NUMBER: LO TELECOMMUNICATION INFORMATION: 617-720-3500
                                                                                                                                                                                                      APPLICATION NUMBER: US 08
FILING DATE: 01-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/C
FILING DATE: 01-SEP-1994
                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/596,291
FILING DATE: 09-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESSE: WOLF, GREENFIELD & SACKS, P.C.
ADDRESSE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2347 HISHLNFTAWPDHDTP 2362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 617/720-3500
                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
                                                                                                                                                  NAME: GATES, EDWARD R. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                            TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/100,804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 HLSILE--AWSDNDTP 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MASSACHUSETTS
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nilarity 56.2%;
Conservative
2465 amino acids
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                                                                                                                                                31,616
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Pred. No. 2.5e
2; Mismatches
                                                                                                                                LO461/7003
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7.5e+02;
3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Watches 9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-080-855-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-080-855-12
                                                                                                                                                                                                                                                                                                                                    PCT-US94-09943-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER APPLICATION NUMBER: 08/805,583
EARLIER FILING DATE: 1997-02-25
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.2
"----hes 9; Conservative
                                                                                                                                                                                                                                                                                                  Sequence 2, Applicating GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gonez, Leonel Jo
APPLICANT: Heldin, Carl-Her
TITLE OF INVENTION: PARG, &
FILE REFERENCE: L0461/7030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Saras, Jan
APPLICANT: Franzn, Petra
APPLICANT: Aspenstrm, Po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/080,855A CURRENT FILING DATE: 1998-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 2466
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
STREET: 600 ATLANTIC
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                   2348 HISHINFTAWPDHDTP 2363
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                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid TOPOLOGY: linear
                                                                                                            CITY: BOSTON
                                                                               COUNTRY:
                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                               4 HLSILE--AWSDNDTP 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gonez, Leonel Jorge
Heldin, Carl-Henrik
                                                                                                                                                                                                                                                                                                                    Application PC/TUS9409943
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                                                                                             MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
 PatentIn Release #1.0,
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56.2%;
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                                                                                                                             AVENUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43; DB
Pred. No. 2.5e
2; Mismatches
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Version #1.25
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3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2466;
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TELERA: 617/720-2441
TELERA: 92-1742 EZEKIEL
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2466 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-09943-2
                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Macrousson, Eric G.
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-0351
CURRENT APPLICATION NUMBER: US/09/290,640
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin Ver. 2.0
EQ ID NO 46
LENGTH: 2485
TYPE: PRT
ORGANISM: Homo sapiens
US-09-290-640-46
Search completed: March 27, 2002; 13:59:29 Job time: 582 sec
                                                                                                                                            δõ
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US-09-290-640-46
Sequence 46, Application US/09290640
Patent No. 6204055
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Best Local Similarity 56.2%;
Matches 9; Conservative
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Best Local Similarity 56.2%;
Matches 9; Conservative
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APPLICATION NUMBER: PCT/US94/09943
FILING DATE: 01-SEP-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: TWOMEY, MICHAEL J:
REGISTRATION NUMBER: P-38,349
REFERENCE/DOCKET NUMBER: LO461/7000WC
TELEPHONE: 617/720-3500
TELEPHONE: 617/720-3500
TELEPAX: 617/720-2441
                                                                                                  4 HLSILE--AWSDNDTP 17
|:| | | | |:|||
2367 HISHLNFTAWPDHDTP 2382
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                                                                                                                                                                                                       Score 43; DB 4; Length 2485; Pred. No. 2.5e+02;
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Pred. No. 2.5e+02;
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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Gapop 10.0 , Gapext 0.5
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119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     March 27, 2002, 14:20:24; Search time 1139.61 Seconds
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/cgn2_6/ptodata/2/paa/US090_COMB.pep:*
/cgn2_6/ptodata/2/paa/US091_COMB.pep:*
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                                                                                                                                                                                                                                                       /cgn2_6/ptodata/2/paa/US085_COMB.pep:*
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/cgn2_6/ptodata/2/paa/US089_COMB.pep:*
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/cgn2_6/ptodata/2/paa/US06_COMB.pep:*
/cgn2_6/ptodata/2/paa/US07_COMB.pep:*
/cgn2_6/ptodata/2/paa/US080_COMB.pep:*
/cgn2_6/ptodata/2/paa/US081_COMB.pep:*
/cgn2_6/ptodata/2/paa/US082_COMB.pep:*
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5.116 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

9	80	7	6	5	4	ω	2	1	No.	Result
75	75	108	108	110	119	119	119	119	Score	
63.0	63.0	90.8	90.8	92.4	100.0	100.0	100.0	100.0	Match	Query
1430	21	21	21	1375	1475	1475	21	21	Match Length DB	
20			16		21		16			
US-09-649-885-2	US-09-290-049-11	US-09-290-049-14	US-09-290-049-12	US-09-740-274-4	US-09-740-274-2	US-09-557-848-2	US-09-290-049-10	US-09-290-049-1	ID	
Sequence 2, Appli	Sequence 11, Appl	Sequence 14, Appl	Sequence 12, Appl	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 10, Appl	Sequence 1, Appli	Description	

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37.8 37.8				38.7	38.7	38.7	38.7	38.7		•				39.1																	
194 236	2603	596	476	476	394	394	2 G	275	199	118	94	62	539	539	330	220	220	196	534	534	178	73	401	391	549	546	340	306	2057	21	1430
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60-215-161-57 US01-14827-98 09-154-750-80	US-60-215-161-7203 US-60-215-161-5891	09-252-991A-2	60-219-23	-US01-22636-9	-09-803-110-88	-09-739-449-882	-195-63	-09-538-092-348	-09-738-626-457	3-395A-22	1-08656-559	-09-417-507-	4-875-	-US01-0	-60-207-422-	-60-229-518-	-60 - 2	-09-595-298A-76	-60-324-109-33	-09-344-882-	-09-867-716-1984	-09-248-796-22	PCT-US01-01309-222	-60-324-109-	-60-324-109-167	-60-324-109-170	-09-595-298A-66	-09-595-298A-66	-499-20	-09-290-049-	US-09-740-274-6
Sequence 5/19, Ap Sequence 9825, Ap Sequence 80, Appl	e 5891,	21255,	Φ,	9, Appl	e 8822		7 0		4571,	e 221,	559	26597	e 762, Ap	762,	equence 75, 1	equence 331,			equence 3314	24, App	equence 19848,	e 2257	222, A	e 20736	equence 16789,	e 17015	uence 660,	nce 66]	2, 7	13, Ap	Sequence 6, Appli

## ALIGNMENTS

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APPLICANT: Smith, Daniel J.
APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: SWITHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARIES
FILE REFERENCE: FDC98-01p2A
CURRENT APPLICATION NUMBER: US/09/290,049
CURRENT FILING DATE: 1999-04-12
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/115,142
EARLIER APPLICATION NUMBER: 60/115,142
EARLIER FILING DATE: 1999-01-08
                    QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1
US-09-290-049-1
                                                                                                                                                             ; OTHER INFORMATION: EAW peptide US-09-290-049-1
                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09290049 GENERAL INFORMATION:
                                                              Matches
                                                                            Query Match
Best Local S
                                                                                                                                                                                             LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                              Local Similarity 100.0%;
1 ANDHLSILEAWSDNDTPYLHD 21
                                                              Conservative
                                                              0
                                                          Score 119; DB 16; Pred. No. 5.3e-11; Wismatches 0;
                                                                                                 Length 21;
                                                              Indels
                                                            0;
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ANDHLSILEAWSDNDTPYLHD

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APPLICANT: Smith, Daniel J.

APPLICANT: Tabbman, Martin A.

TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL

TITLE OF INVENTION: CARIES

FILE REFERENCE: FDC98-0192A

CURRENT APPLICATION, NUMBER: US/09/290,049

CURRENT FILING DATE: 1999-04-12

EARLIER APPLICATION NUMBER: 60/081,550

EARLIER FILING DATE: 1998-04-13

EARLIER FILING DATE: 1998-04-13

EARLIER FILING DATE: 1998-04-13

EARLIER FILING DATE: 1999-01-08

NUMBER OF SEQ ID NOS: 19

SOFTWARE: FSTSSEQ for Windows Version 3.0

SEQ ID NO 10

LENGTH: 21

TYPE: PRT
                       US-09-740-274-2

S-09-740-274-2

; Sequence 2, Application US/09740274

; GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ
SEQ ID NO 2
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Best Local Similarity
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     APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/557,848
CURRENT FILING DATE: 2000-04-26
EARLIER APPLICATION NUMBER: 08/478,704
ARLIER FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Substitutes for Modified Starch
TITLE OF INVENTION: Latexes in Paper Manufacture
                                                                                                                                                                                                                                                                                                                                                                                                                             CARLIER APPLICATION NUMBER: 09/007,999 EARLIER FILING DATE: 1998-01-16 NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1475
TYPE: PRT
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                                                                                                                                                           1 ANDHLSILEAWSDNDTPYLHD 21
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     Nichols, Scott E.
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                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             for Windows Version 3.0
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                                                                                                                                                                                                               100.0%; Score 119; DB 19; 100.0%; Pred. No. 5.2e-09; tive 0; Mismatches 0;
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Pred. No. 5.3e-11;
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; ORGANISM: streptococcus mutans US-09-740-274-4
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SEQ ID NO 2
LENGTH: 1475
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Best Local S
Matches 21
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 4
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                               Matches
                                             Query Match
Best Local Similarity
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PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1000
PRIOR FILING DATE: 1000
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CURRENT FILING DATE: 2000-12-19
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FILE REFERENCE: 0357CRD
                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1998-0
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PRIOR FILING DATE: 1995-06-07
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PRIOR FILING DATE: 1998-12-11
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PRIOR FILING DATE: 1:
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PRIOR APPLICATION NUMBER: 09/0

PRIOR APPLICATION 1998-01-20
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CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 09/210,361
                                                                                                                                                                                                                        PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/009,620 PRIOR FILING DATE: 1998-01-20
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PRIOR FILING DATE: 1995-06-07
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                                                                                                                                                          LENGTH: 1375
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FILING DATE: 1998-01
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                             Conservative
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1998-01-16
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1998-01-16
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                                             92.4%;
95.2%;
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                             0;
                                             Score 110;
Pred. No. 1.
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Pred. No. 5.2
0; Mismatches
                             Mismatches
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                                             2e-07
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.2e-09;
s 0;
                                                           Length 1375;
                               Indels
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507 ANDHLSILEAWSYNDTPYLHD 527

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RESULT 8
US-09-290-049-11
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; ORGANISM: S.
US-09-290-049-14
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; Sequence 11, Application US/09290049
                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: FDC98-01p2A
CURRENT APPLICATION NUMBER: US/09/290,049
CURRENT FILING DATE: 1999-04-12
EARLIER APPLICATION NUMBER: 60/081,550
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/115,142
EARLIER FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 19
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Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Smith, Daniel J.

APPLICANT: Tanbman, Martin A.

APPLICANT: Tanbman, Martin A.

TITLE OF INVENTION: SYMPHETIC PEPTIDE VACCINES FOR DENTAL

TITLE OF INVENTION: CARIES

FILE REFERENCE: FDC98-0192A

CURRENT APPLICATION NUMBER: US/09/290,049

CURRENT FILING DATE: 1999-04-12

EARLIER APPLICATION NUMBER: 60/081,550

EARLIER APPLICATION NUMBER: 60/115,142

EARLIER FILING DATE: 1998-04-13

EARLIER FILING DATE: 1999-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARIES
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APPLICANT:
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nes 18; Conserv
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1 ANNHVSIVEAWSDNDTPYLHD 21
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                                                                                                                                                                            Conservative
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85.7%;
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85.7%;
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Pred. No. 2.7e-09;
3; Mismatches 0;
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2.7e-09;
nes 0;
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US-09-740-274-6
US-09-740-274-6
; Sequence 6, Application US/09740274
; GENERAL INFORMATION:
GENERAL INCIDOLS, Scott E.
; APPLICANT: NICHOLS, Scott E.
; TITLE OF INVENTION: Glucan-containing Compositions and Paper
; FILE REFERENCE: 0357CRD
; CURRENT APPLICATION NUMBER: US/09/740,274
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 09/210,361
; PRIOR FILING DATE: 1998-12-11
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APPLICANT: TAUDMAN, MARTHA A.
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARIES
FILE REFERENCE: FDC98-010-18
CURRENT APPLICATION UMMBER: US/09/290,049
CURRENT FILING DATE: 1999-04-12
EARLIER APPLICATION NUMBER: 60/081,550
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/115,142
EARLIER APPLICATION NUMBER: 60/115,142
EARLIER APPLICATION DATE: 1998-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; SOFTWARE: FastSEQ for Windows V

; SEQ ID NO 2

; LENGTH: 1430

; TYPE: PRT

; ORGANISM: Streptococcus mutans

US-09-649-885-2
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Best Local Similarity 71.4
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/649,885 CURRENT FILING DATE: 2000-08-28 PRIOR APPLICATION NUMBER: US 09/008,172 PRIOR FILING DATE: 1998-01-16 PRIOR APPLICATION NUMBER: 08/482,711 PRIOR FILING DATE: 1995-06-07
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TYPE: PRT
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71.4%;
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71.4%;
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Pred. No. 0.00036;
                                                                                                                                                                                                                                                                                                                                                                                               Score 75; DB 20; Pred. No. 0.034;
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APPLICATION NUMBER: FILING DATE: 1998-

1998-01-16

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US-09-290-049-13
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                                                                                                                  Sequence 2, Application US/09499203 GENERAL INFORMATION:
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Best Local Similarity
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: 60/115,142
EARLIER FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 3.0
BEQ ID NO 13
LENGTH: 21
                                  APPLICANT: KOSSMANN, Jens
APPLICANT: WELSH, Thomas
APPLICANT: QUANZ, Martin
APPLICANT: KNUTH, Karola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, Martin A.
APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARLES
FILE REFERENCE: FDC98-0192A
CURRENT APPLICATION NUMBER: US/09/290,049
CURRENT FILING DATE: 1999-04-12
EARLIER APPLICATION NUMBER: 60/081,550
EARLIER APPLICATION NUMBER: 1516-167
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-13
TITLE OF INVENTION: Nucleic Acid Molecules FILE REFERENCE: 147-196P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: streptococcus
09-740-274-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 08/482,711
PRIOR FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 1430
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FILING DATE: 1998-01-20
APPLICATION NUMBER: 08/485,243
FILING DATE: 1995-06-07
APPLICATION NUMBER: 09/008,172
FILING DATE: 1998-01-16
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FILING DATE: 1995-06-07
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Pred. No. 0.00073;
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US-09-995-298A-661
US-09-995-298A-661
Sequence 661, Application US/09595298A
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              CURRENT APPLICATION NUMBER: US/09/595,298A
CURRENT FILING DATE: 2000-06-16
NUMBER OF SEO ID NOS: 2756
SOFTWARE: PatentIn version 3.0
SEO ID NO 660
LENGTH: 340
TYPE: PRT
                                                                                                                                  GENERAL INFORMATION:
APPLICANT: BALEXANDROV, Nickol
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Sequence-
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-0953P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 2057
TYPE: PRT
                                                                                                                                                                                                                                         Sequence 660, Application US/09595298A
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LENGTH: 306
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Best Local :
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APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Sequence
TITLE OF INVENTION: Thereby
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CURRENT FILING DATE: 2000-02-08
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SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE:
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ORGANISM: Arabidopsis Thaliana
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OTHER INFORMATION: Xaa is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: peptide LOCATION: (1)..(306 OTHER INFORMATION:
ORGANISM: Arabidopsis Thaliana
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11; Conserv
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Pred. No.
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Pred. No.
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; NUMBER OF SEQ ID NOS: 33196
; SEQ ID NO 17015
; LENGTH: 546
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
US-60-324-109-17015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FEATURE:
NAME/KEY: peptide
COATION: (1)..(340)
OTHER INFORMATION: Ceres Seq. ID no. 1026740
NAME/KEY: misc_feature
LOCATION: ()..()
OTHER INFORMATION: Xaa is any aa, unknown or other
US-09-595-298A-660
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Search completed: March 27, 2002, 14:20:24 Job time: 1571 sec
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Best Local Similarity 52.9

Matches 9; Conservative
                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cao, Yongwei
APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Stein, Joshua
TITLE ON TUNENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)B
CURRENT APPLICATION NUMBER: US/60/324,109
CURRENT FILING DATE: 2001-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60-324-109-17015
equence 17015, Application US/60324109
ENERAL INFORMATION:
                                                                                                   2 NDHLSILEAWSDNDTPY 18
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144 NDELAALETW-DNGKPY 159
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234 DYEQIMEAWSDKGTLYV 250
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52.9%;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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aximum DB
     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*

8: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
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length: 2000000000
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Match
   US-09-290-049A-10
119
1 ANDHLSILEAWSDND
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-562-328-20
US-09-290-049A-11
US-09-290-049A-11
US-09-562-328-23
US-09-562-328-23
US-09-562-328-25
US-09-562-328-22
US-09-290-049A-14
US-09-562-328-22
US-09-563-328-22
US-09-563-328-23
US-09-563-328-24
US-09-563-328-24
US-09-564-957-5
US-09-604-957-5
US-09-708-427-55325
US-09-708-427-7993
US-09-604-957-7
US-09-604-957-3
US-09-604-957-3
US-09-604-957-3
US-09-604-957-3
US-09-604-957-3
US-09-708-427-7993
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               20, Appli 10, Appli 21, Appli 22, Appli 22, Appli 22, Appli 24, Appli 25, Ap
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RESULT 2 US-09-290-049 Sequence 1, GENERAL INF APPLICANT: APPLICANT: TITLE OF I TITLE OF I TITLE REFER CURRENT FI PRIOR APPL PRIOR FILL; P	Query Match Best Local Matches 2  Qy 1 AND      Db 1 AND	RESULT 1 US-09-562-328 Sequence 20 GENERAL INF APPLICANT: APPLICANT: APPLICANT: TITLE OF I FILE REFER CURRENT FI PRIOR APPL PRIOR APPL PRIOR APPL PRIOR OF LENGTH: 2 SEQ ID NO 2 LENGTH: 2 TYPE: PRI ORGANISM: ORGANISM: ORGANISM:		26 27 28 29 31 31 32 33 33 34 44 41 41 41 41 41 41 41 41 41 41 41 41
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US/09290049A  I. J.  II. J.  II. J.  III. J.  II	;; Score 119; DB 6; Length ;; Pred. No. 2.9e-12; 0; Mismatches 0; Indels 21	/09562328 N. A. TE 'VACCINES FOR THE PREVENTION -01 -01 -01 -01 -01 -01 -01 -01 -01 -01	ALIGNMENTS	US-10-067-649-90 US-09-708-427-27416 US-09-708-427-27414 US-09-808-615-73 US-09-605-703B-2226 US-09-897-516-7293 US-09-897-516-779 US-09-897-516-5719 US-09-897-516-5719 US-09-154-750A-80 US-09-708-427-25322 US-09-815-242-11634 US-10-072-851-110188 US-09-815-242-10188 US-09-815-242-10188
f- ·	.h 21; .ls  0; Gaps  0	OF DENTAL CARIES		Sequence 90, Appl Sequence 27415, A Sequence 27414, A Sequence 77, Appl Sequence 7203, Appl Sequence 5719, Appl Sequence 5719, Appl Sequence 80, Appl Sequence 25321, A Sequence 25321, A Sequence 11634, A

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SOFTWARE: FastSEQ for Windows Version

4.0

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; ORGANISM: Streptococcus sp
US-09-562-328-21
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Best Local Similarity 100.
21; Conservative
                                                       SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 21
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                                                                                                               APPLICANT: LEES, ANDREW
APPLICANT: TAUBMAN, MARTIN A.
APPLICANT: SMITH, DANIEL J.
TITLE OF INVENTION: CONJUGATE VACCINES FOR THE PREVENTION OF DENTAL CARIES
FILE REFERENCE: 04995.0046-01
CURRENT APPLICATION NUMBER: US/09/562,328
CURRENT FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 09/288,965
PRIOR APPLICATION NUMBER: 09/288,965
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 44
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PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
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APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: SYMTHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARIES
FILE REFERENCE: 1564.1008-002
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Pred. No. 2.9e-12;
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RESULT 7 US-09-290-049A-12

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PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
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SEQ ID NO 23
LENGTH: 21
TYPE: PRT
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Best Local Similarity
Matches 18; Conserv
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Best Local :
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Best Local Similarity
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PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 44
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                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/C
CURRENT FILING DATE: 2000-05-01
                                                                                                                                                                                                                                                                                                               APPLICANT: SMITH, DANIEL J.
TITLE OF INVENTION: CONJUGATE VACCINES FOR THE PREVENTION OF DENTAL CARIES FILE REFERENCE: 04995.0046-01
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nes 18; Conserv
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ANNHVSIVEAWSDNDTPYLHD
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Pred. No. 7.4e-11;
                                                                          Score 108; DB 6;
Pred. No. 1.5e-10;
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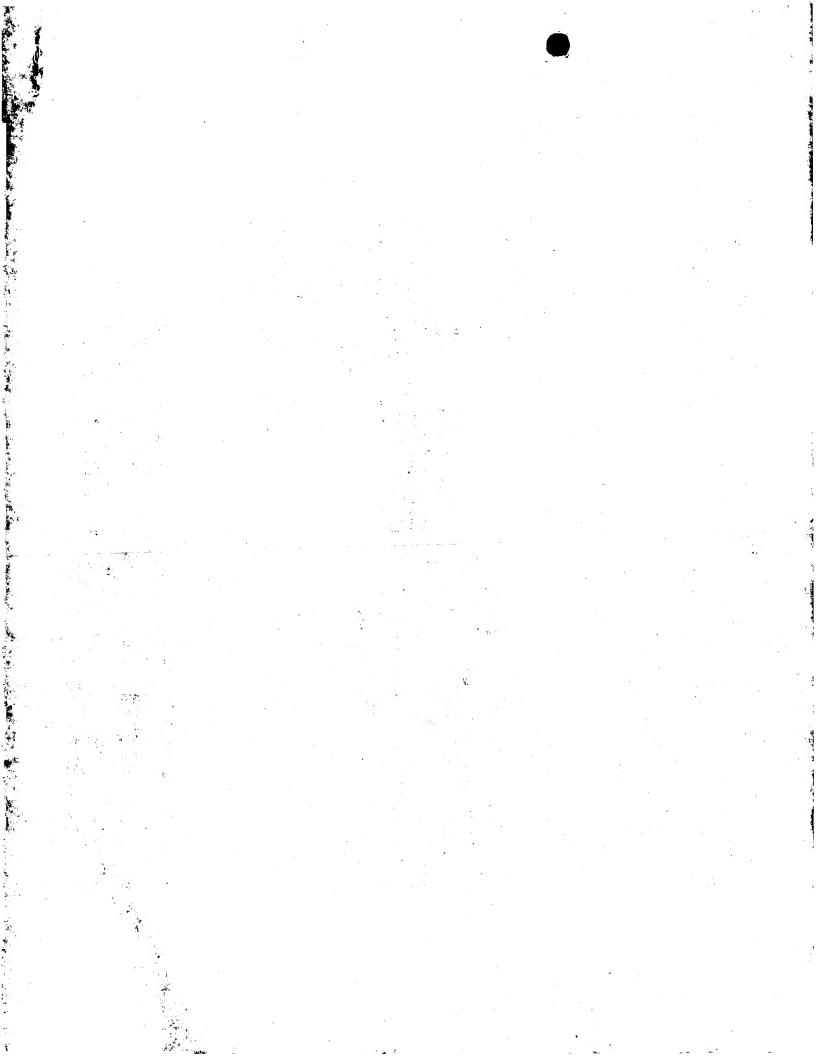
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US-09-290-049A-14
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Sequence 22, Application US/09562328
GENERAL INFORMATION:
APPLICANT: LEES, ANDREW
APPLICANT: TAUBMAN, MARTIN A.
APPLICANT: SMITH, DANIEL J.
APPLICANT: SMITH, DANIEL J.
TITLE OF INVENTION: CONJUGATE VACCINES FOR THE PREVENTION OF DENTAL CARIES FILE REFERENCE: 04995.0046-01
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 14
LENGTH: 21
TYPE: PRT
ORGANISM: S. sobrinus
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Best Local S
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TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARIES
FILE REFERENCE: 1564.1008-002
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CURRENT FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 19
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APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARLES
FILE REFERENCE: 1564.1008-002
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ORGANISM: S. downei
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85.7%;
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Pred. No. 1.5e-10;
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SOFTWARE: FASTSEQ for SEQ ID NO 11
LENGTH: 21
TYPE: PRT
ORGANISM: S. mutans
US-09-290-049A-11
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LENGTH: 21
TYPE: PRT
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Best Local Similarity 71.4
Matches 15: Conservative
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Best Local Similarity 71.4%;
Matches 15; Conservative
SEQ ID NO 4
                                                                              APPLICANT: RAHAOUI, HAKIM
APPLICANT: LEER, ROBERT JAN
TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASE AND NOVEL GLUCAN
FILE REFERENCE: BO 43388
CURRENT APPLICATION NUMBER: US/09/604,957
CURRENT FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 00201871.1
PRIOR APPLICATION STATE: 2000-05-25
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA APPLICANT: DIJKHUIZEN, LUBBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/290,049A CURRENT FILING DATE: 1999-04-12 PRIOR APPLICATION NUMBER: 60/081,550 PRIOR FILING DATE: 1998-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARIES
FILE REFERENCE: 1564.1008-002
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SOFTWARE: PatentIn Ver. 2.1
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                                         SOFTWARE: PatentIn Ver. 2.1
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Pred. No. 2.3e-05
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Pred. No. 2.
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                                                                                                                                                                    US-09-290-049A-13
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APPLICANT: SMITH, DANIEL J.
TITLE OF INVENTION: CONJUGATE VACCINES FOR THE PREVENTION OF DENTAL CARIES
FILE REFERENCE: 04995.0046-01
CURRENT PAPLICATION NUMBER: US/09/562,328
CURRENT FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 09/288,965
PRIOR APPLICATION NUMBER: 09/288,965
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 44
SOETWARE: PATENTIN VET. 2.1
SEQ ID NO 24
LENGTH: 21
THE OF THE 
                                                                                                                                                                                                                                       SEQ ID NO 13
LENGTH: 21
TYPE: PRT
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Best Local Similarity
Matches 14; Conserv
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Best Local :
                               Query Match
Best Local Similarity
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APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARIES
FILE REFERENCE: 1564.1008-002
Matches
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                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/290,049A
CURRENT FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 19
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Pred. No. 0.00094;
1; Mismatches 5;
                               Score 73; DB 6;
Pred. No. 4.7e-05;
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Pred. No. 4.7e-05;
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: TYPE: PRT : ORGANISM: Leuconostoc mesenteroides US-09-604-957-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/09604957 GENERAL INFORMATION:
                                                                   Query Match
Best Local Similarity 55.0
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 5
                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                           APPLICANT: RAHAOUI, HAKIM
APPLICANT: LEER, ROBERT-JAN
APPLICANT: LEER, ROBERT-JAN
TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASE AND NOVEL GLUCAN
FILE REFERENCE: BO 43388
FILE REFERENCE: BO 43388
CURRENT APPLICATION NUMBER: US/09/604,957
CURRENT FILING DATE: 2000-06-28
CURRENT FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 00201871.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: RAHAOUI, HAKIM
APPLICANT: LEER, ROBERT-JAN
TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASE AND NOVEL GLUCAN
FILE REFERENCE: BO 43388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/604,957
CURRENT FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 00201871.1
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                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA APPLICANT: DIJKHUIZEN, LUBBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 0020 PRIOR FILING DATE: 2000-05-25
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                                                                                                                                                                                                                               LENGTH: 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 ANOHLSILEDWSHNDPLYVTD 95
 75
                                     1 ANDHLSILEAWSDNDTPYLH 20
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ANKHLSILEDWNGKDPQYVN 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
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                                                                                               50.4%;
55.0%;
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66.7%;
                                                                           ω
                                                                                               Score 60; DB 6
Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 71; DB 6;
Pred. No. 0.0038;
                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 6; Length 523;
                                                                                                                 DB 6;
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                                                                                                                 Length 584;
                                                                           Indels
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Search completed: March 27, 2002, 14:22:47 Job time: 1694 sec



Run on: OM protein - protein search, using sw model March 27, 2002, 14:01:17; Search time 102.51 Seconds (without alignments) 15.605 Million cell updates/sec GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

Title: Perfect score: US-09-290-049A-10 119 1 ANDHLSILEAWSDNDT

Sequence: ANDHLSILEAWSDNDTPYLHD 21

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 219241 segs, 76174552 residues

tal number of hits satisfying chosen parameters: 219241

imum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_68:\*

<u>\*</u> 3: 2: pir1:\*
pir2:\*
pir3:\*
pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	w	2	1	No.	Result
45	45.5	46	46	46	46	47	47	47	47	47.5	47.5	48	49	49.5	50	52	57	57	58	63	66	66	74	75	78	108	110	119	Score	
37.8	38.2	38.7	38.7	38.7	8	9.	9.	39.5	9	9.	9		41.2	41.6	42.0	43.7	47.9	47.9	•	52.9	٠		•		•		•	100.0		% Query
236	96	476	335	335	275	525	524	378	175	519	331	490	336	549	347	4848	1599	331	1518	1577	1449	1449	1508	1431	1365	1592	1375	1475	Length	
2	Ν	ب	2	N	N	N	N	N	2	N	ш	N	Н	2	N	N	N	2	2	2	2	2	N	2	2	2	N	2	DB	
S62732	E81786	S58229	B72053	E86568	S55978	T40088	D82220	T04254	C86205	C86372	DEUTGC	H70538	QQBE40	T03983	T48610	T30289	S22737	B48445	A44811	T30858	T30552	T30857	T31098	A45866	A41483	A38175	JT0345	в33135	ID	
guanidinoacetate N	conserved hypothet	άŽ	glyceraldehyde 3-p	qlyceraldehyde-3-P	hypothetical prote	RhoGEF domain cont	~			hypothetical prote	glyceraldehyde-3-p	pr	BGLF2 protein - hu	н	hypothetical prote	pristinamycin I sy	glucosyltransferas	glyceraldehyde-3-p	glucosyltransferas	glucosyltransferas	glucosyltransferas	glucosyltransferas	Ω.	dextransucrase (EC	glucosyltransferas	OD.	dextransucrase (EC	gtfB protein precu	cription	

dextransucrase (EC 2.4.1.5) precursor - Streptococcus mutans (strain GS-5) N;Alternate names: sucrose 6-glucosyltransferase C;Species: Streptococcus mutans C;Species: Streptococcus mutans C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 24-Sep-1999 C;Accession: JT0345; C33135 R;Udda, S.; Shiroza, T.; Kuramitsu, H.K. Gene 69, 101-109, 1988 A;Title: Sequence analysis of the gtfC gene from Streptococcus mutans GS-5. A;Reference number: JT0345; MUID:89137980

RESULT

5	44	3	42	41	0	39	38	37	36	ω 5	34	ω	32	31	30
43.5	44	44	44	44	44	44	44	44	44	44	44	44	44.5	45	45
36.6	37.0	37.0	37.0	37.0	37.0	37.0	37.0	37.0	37.0	37.0	37.0	37.0	37.4	37.8	37.8
97	1313	1208	468	436	337	337	337	333	333	331	331	247	210	1159	947
2	N	N	N	N	_	_	_	N	ш	N	Н	N	2	2	Ν
S12958	T29027	в82091	S61964	T24953	DEBHG	DEZMGC	DEJJGC	JC5370	DECHG3	D85788	DEECG3	PQ0178	н83332	T43461	E86362
tachykinin delta p	hypothetical prote	exodeoxyribonuclea	probable membrane	hypothetical prote	glyceraldehyde-3-p	glyceraldehyde-3-p	glyceraldehyde-3-p	glyceraldehyde~3-p	glyceraldehyde-3-p	glyceraldehyde-3-p	glyceraldehyde-3-p	glyceraldehyde-3-p	conserved hypothet	probable phosphodi	hypothetical prote

# ALIGNMENTS

QY 1 ANDHLSILEAWSDNDTPYLHD 21 	Query Match 100.0%; Score 119; DB 2; Length 1475; Best Local Similarity 100.0%; Pred. No. 3.9e-10; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	submitted to the Protein Sequence Database, September 1990 A;Reference number: A33128 A;Rccession: A33128 A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA A;Residues: 1-171,173-641,'N',643-1475 <sh2> A;Experimental source: strain GS-5 C;Superfamily: cpl repeat homology <cp1> F;1056-1115/Domain: cpl repeat homology <cp2> F;1224-1243/Domain: cpl repeat homology <cp3> F;1289-1308/Domain: cpl repeat homology <cp4> F;1289-1373/Domain: cpl repeat homology <cp4> F;1354-1373/Domain: cpl repeat homology <cp5> F;1419-1438/Domain: cpl repeat homology <cp5></cp5></cp5></cp4></cp4></cp3></cp2></cp1></sh2>	R;Shiroza, T.; Ueda, S.; Kuramitsu, H.K.  J. Bacteriol. 169, 4263-4270, 1987  A;Title: Sequence analysis of the 9tfB gene from Streptococcus mutans.  A;Reference number: A33135; MUID:87308013  A;Accession: B33135  A;Status: preliminary  A;Molecule type: DNA  A;Residues: 1-1475 <shi> A;Residues: 1-1475 <shi> A;Cross-references: GB:M17361; NID:9153639; PIDN:AAA88588.1; PID:9153640  R;Shiroza, T.; Ueda, S.; Kuramitsu, H.K.</shi></shi>	RESULT 1  B33135  gtfB protein precursor - Streptococcus mutans C;Species: Streptococcus mutans C;Date: 23-Oct-1990 #sequence_revision 23-Oct-1990 #text_change 15-Oct-1999 C;Accession: B33135; A33128
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F;1093-1112/Domain: cpl repeat homology <CF;1221-124/Domain: cpl repeat homology <CF;1287-1306/Domain: cpl repeat homology <CF;1287-1306/Domain: cpl repeat homology <CF;1330-1351/Domain: cpl repeat homology <CF;1352-1371/Domain: cpl repeat homology <CF;1402-1420/Domain: cpl repeat homology <CF;1465-1464/Domain: cpl repeat 
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Keywords: duplication; glycosyltransferase; hexosyltransferase
-34/Domain: signal sequence #status predicted <SIG>
55-1375/Product: glucosytransferase #status predicted <MAT>
F;1126-1145/Domain: cpl repeat homology <CP1>
F;1253-1272/Domain: cpl repeat homology <CP2>
F;1318-1337/Domain: cpl repeat homology <CP3>
                                                                       RESULT
A41483
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R;Shiroza, T.; Ueda, S.; Kuramitsu, H.K.
J. Bacteriol. 169, 4263-4270, 1987
A;Title: Sequence analysis of the gtfB gene
A;Reference number: A33135; MUID:87308013
A;Accession: C33135
glucosyltransferase
C; Species: Streptoco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glucosyltransferase precursor - Si
C; Species: Streptococcus sobrinus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Abo, H.; musuman, 989-996, 1991
J. Bacteriol. 173, 989-996, 1991
A;Title: Peptide sequences for sucrose splitting
A;Title: Peptide sequences for sucrose splitting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: A38175
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A; Residues: 1-349 <SHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
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A; Residues: 1-1375 < UED>
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Best Local Similarity
Matches 20; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: GB:D90213; NID:g217032; PIDN:BAA14241.1; Superfamily: cpl repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics:
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kesidues: 1-1592 <ABO>
                                                                                                                                                                                                                        477 ANNHVSIVEAWSDNDTPYLHD 497
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   Streptococcus
                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                catalyzes the synthesis of both water-soluble and water-insoluble glucans cpl repeat homology
                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                     (EC
                                 2.4.1.-)
                                                                                                                                                                                                                                                                                                                                                                                                    90.8%;
85.7%;
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95.2%;
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                                 gtfS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T.; Ohta, H.; Fukui, K.; Kato, K.; Kagawa, H
                                                                                                                                                                                                                                                                                                                                                                   ω
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 108; DB 2; Pred. No. 2.2e-08;
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Pred. No. 9.
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                                     precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <CP1>
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<CP3>
<CP4>
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.1e-09;
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                                     Streptococcus sobrinus
                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1592;
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A; Cross-references: GB:M29296
C; Superfamily: cpl repeat homology
C; Keywords: glycosyltransferase; hexosyltransfer
F;181-201/Domain: cpl repeat homology <CPl>
F;1197-1146/Domain: cpl repeat homology <CP2>
F;1197-1211/Domain: cpl repeat homology <CP3>
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F;1341-1361/Domain: cpl repeat homology <CP7>
C;Accession: T31098
C;Accession: T31098
R;Monchois, V.; Remaud-Simeon, M.; Monsan, FEMS Microbiol. Lett. 159, 307-315, 1998
A;Title: Cloning and sequencing of a gene A;Title: Cloning and sequencing of a gene A;Accession 
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A;Molecular
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C;Keywords: gly
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                                                                                                                                                                       probable dextransucrase (EC 2.4.1.5), extracellular - Leuconostoc mesenteroides C;Species: Leuconostoc mesenteroides C;Date: 22-Oct.1999 #sequence_revision 22-Oct.1999 #text_change 11-May-2000 C;Accession: T31098
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A;Residues: 1-1365 <GTL>
A;Cross-references: GB:M30943; NID:g153652;
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A; Gene: gtfS
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A; Residues: 1-1431 <HON>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R:Honda, O.; Kato, C.; Kuramitsu, H.K. J. Gen. Microbiol. 136, 2099-2105, 199
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glycosyltransferase; hexosyltransferase
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Pred. No. 0.00087;
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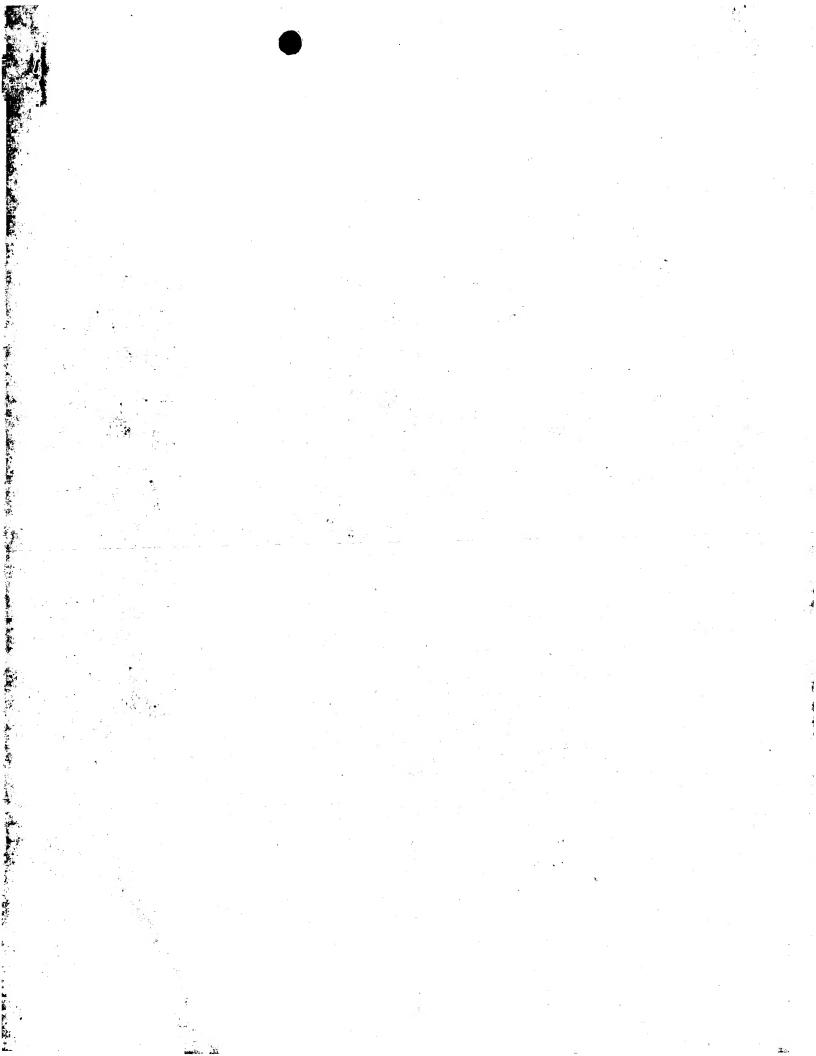
HLSILEAWSHNDAYYNED

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A;Cross-references: EMBL:AF049609; NID:g2935545; PID:g2935546; C;Genetics: A;Gene: gtfN
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A;Gene:
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A;Residues: 1-1508 <MON>
A;Residues: 1-1508 <MON>
A;Cross-references: EMBL:AF030129; NID:g2766611; PID:g2766612; PIDN:AAB95453.1
A;Experimental source: strain NRRL B-1299
C;Genetics:
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                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, February 1998 A; Description: Streptococcus salivarius V1477 gtfN.
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R;Jaffe, R.I.
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                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-1449 <
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A; Accession: T30552
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A; Residues: 1-1449 <SIM>
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C; Function:
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Species: Streptococcus salivarius
Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Genetics:
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Species: Streptococcus salivarius
Date: 22-Oct-1999 #sequence_revision 22-Oct-1999
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13; Conser
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                                             Score 66; DB Pred. No. 0.06 0; Mismatches
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Pred. No. 0.0041;
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             glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Leishmania mexicana (Species: Leishmania mexicana C;Species: Leishmania mexicana C;Species: Leishmania mexicana C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 11-Jun-1999 C;Accession: B48445; S25142
R;Hannaert, V: Blaauw, M.; Kohl, L.; Allert, S.; Opperdoes, F.R.; Michels, P.A.M.
Mol. Biochem. Parasitol. 55, 115-126, 1992
A;Title: Molecular analysis of the cytosolic and glycosomal glyceraldehyde-3-phosphat A;Reference number: A48445; MUID:93063042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glucosyltransferase (EC 2.4.1.-) I - Streptococcus salivarius C;Species: Streptococcus salivarius C;Species: Streptococcus salivarius C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 15-Oct-1999 C;Accession: A44811; S22726; S28809 R;Giffard, P.M.; Simpson, C.L.; Milward, C.P.; Jacques, N.A. J. Gen. Microbiol. 137, 2577-2593, 1991 A;Title: Molecular characterization of a cluster of at least two glucosyltra A;Reference number: A44811; MUID:92148377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: cpl repeat homology
C;Keywords: glycosyltransferase; hexosyltransferase
F;1307-1326/Domain: cpl repeat homology <CP4>
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A; Reference number: A; Accession: B48445
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C; Accession: T30858
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C; Species: Streptococc
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A; Residues: 1-1577 <SIM>
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C:Species: Streptococcus salivarius
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: S22737; S28810; B44811; S22727
R:Jacques, N.
submitted to the EMBL Data Library, March 1992
A:Reference number: S22726
A:Reference number: S22726
A:Accession: S22737
A:Accession: S22737
A:Molecule type: DNA
A:Residues: 1-1599 <JAC>
A:Cross-references: EMBL:Z11872; NID:g47530; PIDN:CAA77898.1; PID:g47531
A:Experimental source: ATCC 25975
R:Giffard, P.M.; Simpson, C.L.; Milward, C.P.; Jacques, N.A.
J. Gen, Microbiol. 137, 2577-2593, 1991
A:Title: Molecular characterization of a cluster of at least two glucosyltransferase gen A:Reference number: A44811; MUID:92148377
A:Accession: S28810
R;de Crecy-Lagard, V.A.; Saurin, W.; Thibaut, D.; Gil, P.; Naudin, L.; Crouzet, submitted to the EMBL Data Library, February 1997
A;Description: Streptogramin B biosynthesis in Streptomyces pristinaespiralis an A;Reference number: Z20808
A;Reference number: Z20808
A;Recession: T30289
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4848 <DEC>
A;Cross-references: EMBL:Y11548; NID:e1025755; PID:e307539; PIDN:CAA72312.1
C;GenetLog:
A;Gene: snbDE
C;Superfamily: acyl carrier protein homology; acetate--CoA ligase homology
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c;Species: Streptomyces pristinaespiralis
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 01-Dec-2000
C;Accession: T30289
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A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-331 <HAN>
A:Cross references: EMBL:X65220; NID:g9552; PIDN:CAA46323.1; PID:g9553
C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C:Keywords: oxidoreductase
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C;Superfamily: cpl repeat homology
C;Keywords: glycosyltransferase; hexosyltransferase
F;1456-1475/Domain: cpl repeat homology <CPR>
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C; Genetics:
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C:Keywords: carrier protein; phosphopantetheine; phosphoprotein F;511-951/Domain: acetate--CoA ligase homology <ACLI>F;966-1034/Domain: acetate--CoA ligase homology <ACPI>F;966-1034/Domain: acetate--CoA ligase homology *ACPI>F;1563-2024/Domain: acetate--CoA ligase homology *ACPI>F;2399-2467/Domain: acyl carrier protein homology <ACPI>F;2399-3427/Domain: acetate--CoA ligase homology <ACCI3>F;2995-3427/Domain: acyl carrier protein homology <ACCI3>F;39441-3509/Domain: acyl carrier protein homology <ACPI>F;4507-4575/Domain: acetate--CoA ligase homology <ACPI>F;4507-4575/Domain: acyl carrier protein homology <ACPI
A;Map position: 9
A;Note: rf2
C;Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology
F;107-370/Domain: aldehyde dehydrogenase homology <ALD>
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A;Title: The rf2 nuclear restorer gene of A;Reference number: Z15177; MUID:96243131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Zea mays (maize)
C;Date: 23-Apr-1999 #sequence_revision
C;Accession: T03983
                                                                                                                                             A; Experimental C; Genetics:
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A; Residues: 1-549 <CUI>
A; Cross-references: EMBI
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Introns: 232/3;
A; Note: F18022.160
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A; Residues: 1-347 <BEV>
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A;Accession: T48610
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
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G3P_BOVIN
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G3P1_ECOLI
G3P_CHICK
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P27470 streptococc
P11001 streptococc
P29336 streptococc
P49331 streptococc
Q01558 leishmania
P03221 epstein bar
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8 leisimania
1 epstein-bar
7 trypanosoma
1 saccharomyc
0 chlamydia p
8 pseudomonas
3 homo sapien
9 fusarium ox
4 streptomyce
2 meleagris g
7 escherichia
6 columba liv
5 zea mays (m
7 hordeum vul
9 cryphonectr
4 jaculus ori
16 zea mays (m
0 oryctolagus
1 mesocricetu
9 mus musculu
7 rattus norv
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P40566 saccharomyc		P22992 escherichia		Q12923 homo sapien						P00355 sus scrofa	

#### ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).  EMBL; M17361; AAA888588.1; EMBL; D88651; BAA26101.1;	GTFB_STRMU  GTFB_STRMU  P08987; 069381; 069384; 069387; 01-NOV-1988 (Rel. 09, Created) 15-JUL-1999 (Rel. 38, Last sequ 15-JUL-1999 (Rel. 38, Last anno GLUCOSYLTRANSFERASE) STREPLOCOCCUS mutans. Bacteria; Firmicutes; Bacillus/ STRAIN=GS-5; MEDLINE-87308013; PubMed=304068 STRAIN=6S-5; MEDLINE-87308013; PubMed=304068 SHIFT STRAIN=103-15; Kuramitsu "Sequence analysis of the 9tfb J. Bacteriol. 169:4263-4270(198 [2] SEQUENCE FROM N.A. STRAIN=MT4239, MT4245, MT4251, MEDLINE-98231643; PubMed=957012 FUJIWATA T., Terao Y., Hoshino Kimura S., Hamada S.; "MOLECULAR analyses of glucosyl Streptococcus mutans."; TOURTION: PRODUCTION OF EXT TO PLAY A KEY ROLE IN THE D AGGREGATION OF BACTERIAL CE 1- CATALYTIC ACTIVITY: SUCROSE D-FRUCTOSE + (1,6-ALPHA-D-G 1- SUBCELLULAR LOCATION: SECRE 1- ALINEED GLUCANS SIMILARITY: TO OTHER GLUCOS BINDING PROTEIN FROM S.MUTA  SIMILARITY: TO OTHER GLUCOS BINDING PROTEIN FROM S.MUTA  SIMILARITY: TO OTHER GLUCOS BINDING PROTEIN FROM S.MUTA	LT 1

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InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 13.
Pfam; PF02324; Glyco_hydro_70; 1.
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481
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; D88660; BAA26113.1;
; D89977; BAA26119.1;
B33135; B33135.
            ANDHLSILEAWSDNDTPYLHD
ANDHLSILEAWSDNDTPYLHD 501
                                                             Similarity
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ilarity 100.
Conservative
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AA; 165685
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CATALYTIC (APPROXIMATE).
GLUCAN-BINDING (APPROXIMATE).
A REPEAT.
S X TANDEM REPEATS.
                                                                                                                                                     ADQDVRVAASTAPSTDGK
                                                              Score 119;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                             IN REF. 1).
-> L (IN REF. 1).
; 3479B62B07694D98
                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal; Repeat; Dental caries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T (IN STRAIN MT4239), MT
T (IN STRAINS MT4239), MT
$11, MT4467 AND MT8148).
V (IN STRAIN MT4239).
P (IN STRAIN MT4251).
I (IN STRAIN MT4251).
F (IN STRAIN MT4251).
N (IN STRAIN MT4251).
N (IN STRAIN MT4231).
S (IN STRAIN MT4239, MT
                                                                                                                                                                                                                                                                                                                                                                                                ADS (IN STRAINS MT4245, MT4251 AND
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N STRAINS
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STRAINS
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STRAIN M
REF. 1).
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s 0;
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NS MT4245
NMT4467).
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MT4245
MT4239,
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                                                                        Length 1476;
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                                                 Indels
                                                                                                                CRC64;
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                                                                                                                                                                                                                              AND MT4251).
AND MT4251).
MT4245, MT42
                                                                                                                                                                                          AND
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                                                Gaps
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ID GTFC_S

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CG GLUCOS

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CG STRAIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTEC_STRMU STANDARD; PRT; 1375 AA. P13470; P05427; 01-NOV-1988 (Rel. 09, Created) 01-JAN-1990 (Rel. 13, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) GLUCOSYLTRANSFERASE-SI PRECURSOR (EC 2.4.1.5)
                       DOMAIN
REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                   InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70
Pfam; PF01473; CW_binding_1; 7.
Pfam; PF02324; Glyco_hydro_70; 1.
                                                                                                                                                                                                                                                                                                                                      EMBL; M22054; AAA88592.1; -.
EMBL; M17361; AAA888899.1; -.
EMBL; JT0345; JT0345
PIR; JT0345; C33135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-89137980; PubMed=2976010; Ueda S., Shiroza T., Kuramitsu H.K.; "Sequence analysis of the gtfC gene Gene 69:101-109(1988).
                                                                                                                                                                                                              Transferase;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus.
NCBI_TaxID=1309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DEXTRANSUCRASE)
GTFC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISEASE: DENTAL CARIES.

MISCELLANEOUS: GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES AND BINDING PROTEIN FROM S.MUTANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FORMS OF GLUCANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Firmicutes;
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                                                                                                                                                                                                                                    Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SUCROSE 6-GLUCOSYLTRANSFERASE).
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1200
1200
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    153022
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                                                          GLUCOSYLTRANSFERASE-SI.
CATALYTIC (APPROXIMATE).
GLUCAN-BINDING (APPROXIMA
2.4 A, 1 C AND 1 AC REPEAT
A REPEAT.
A REPEAT.
C REPEAT.
  AC REPEAT.
A REPEAT (INCOMPLETE).
MW; D4B80CBEE0AACE13 CRC64;
                                                                                                                                                                                                                                Signal; Repeat; Dental caries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       There are no resing as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus mutans GS-5.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                         (APPROXIMATE)

1 AC REPEATS.
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GTF2_STRDO
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1992
01-AUG-1992
15-DEC-1998
                                                                                                                                                                                                                                                         between
the Euro
                                 DOMAIN
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DOMAIN
                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1992 (Rel. 23, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GLUCOSYLTRANSFERASE-I PRECURSOR (EC 2.4.1.5)
           REPEAT
REPEAT
                                                                                                                                                                                                       modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus sobrinus synthetase).";
J. Bacteriol. 173:989-9-1:- FUNCTION: PRODUCTIO
                                                                                                                                                         PIR; A38175; A38175.
HSSP; P00695; 2HEE.
                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTF2_STRDO
P27470;
                                                                      CHAIN
                                                                                                          Pfam;
                                                                                                                                InterPro; IPR002479; InterPro; IPR003318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kagawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91123227; PubMed=1704006; Abo H., Matsumura T., Kodama T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=6715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus downei (Streptococcus sobrinus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Peptide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SUCROSE 6-GLUCOSYLTRANSFERASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteriol. 173:989-996(1991)
                                                                                                                                                                                                                                                                                                                                          MISCELLANEOUS: GTF-I SYNTHESIZES WATER-INSOLUBLE (
1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S:
WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI
                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT TO PLAY A KEY ROLE IN THE DEPLOPMENT OF THE DENTAL PLAQUE BECAPOP THEIR ABILITY TO ADHERE TO SMOOTH SUFFACES AND MEDIATE THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N) =
                                                                                                                                                                                                                                                       European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                       SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES BINDING PROTEIN FROM S.MUTANS.
                                                                                                                                                                                                                                                                                                                                                                                DISEASE: DENTAL CARIES.
                                                                                                                                                                                                                                                                                                                                                                                            D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).
SUBCELLULAR LOCATION: SECRETED.
                                                                                                                                                                                                                                                                                                                                FORMS OF GLUCANS
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                                                                                                       D90213;
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                                                                                            Glycosyltransferase; Signal;
                                                                                                                                                                                  BAA14241.1;
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95.2%;
                                                                                                                                           CW_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus/Clostridium group; Streptococcaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sucrose splitting and glucan binding glucosyltransferase (water-insoluble
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                                POTENTIAL.
GLUCOSYLTRANSFERASE-I.
GLUCATALYTIC (APPROXIMATE).
GLUCAN-BINDING (APPROXIMATE).
6.5 X TANDEM REPEATS.
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                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                       There
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                                                                                                                                                                                                                                           as its content
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                                                                                             Repeat;
                                                                                                                                                                                                                             Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GTF-I) (DEXTRANSUCRASE)
                                                                                                                                                                                                                                                                                                                  AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1375;
                                                                                                                                                                                                                                                                                                                   SOME
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                                                                                                                                                                                                                                                                                                                                                        GLUCANS (ALPHA
SYNTHESIZES
                                                                                                                                                                                                                                                       restrictions
                                                                                                                                                                                                                                                                                                                                           SYNTHESIZES
                                                                                                                                                                                                                                                                                                                   TO
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                                                                                              caries
                                                                                                                                                                                                                                                                                                                   A GLUCAN
                                                                                                                                                                                                                                                                               a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glucan
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commercial
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RESULT 4
GTF1_STRDO
ID GTF1_STRDO
AC P11001;
DT 01-JUL-1989
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Best Local
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                "Nucleotide sequence of a glucosyltransferase sobrinus MFe28.";
             DOMAIN
DOMAIN
                                               SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GLUCOSYLTRANSFERASE-I PRECURSOR (EC 2.4.1.5)
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REPEAT
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                                                                                        EMBL; MI/391; ANCOUNT INTERPRO 1 PRO02479; CW_binding. InterPro; IPR003318; Glyco_hydro_70.
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                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriol. 169:4271-4278(1987).
- FUNCTION: PRODUCTION OF EXTRACELLULAR
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DISEASE: DENTAL CARIES.

MISCELLANEOUS: GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA I,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BY
                                                                                                                                                                                                                                                                                                                                                AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N)

D-FROCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).
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                                                                                 PF01473; CW_binding_1;
PF02324; Glyco_hydro_7
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1.25 A, 2 B, AND 5 AC A REPEAT.
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PIR; A41483; A41483.

R InterPro; IPR002479; CW_binding.

R InterPro; IPR003318; Glyco_hydro_70.

DR Pfam; PF01473; CW_binding_1; 10.

DR Pfam; PF02324; Glyco_hydro_70; 1.

DR Pfam; PF02324; Glyco_hydro_70; 1.

OR 37 (POTENTIAL).

1 36 GLUCOSYLTRANSFERASE-S.
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01-DEC-1992 (Rel. 2
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"Analysis of the Streptococcus downel gtfS gene, which
glucosyltransferase that synthesizes soluble glucans.";
Infect. Immun. 58:2452-2458(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Streptococcus.
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01-DEC-1992 (Rel. 24, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
GLUCOSYLTRANSFERASE-S PRECURSOR (EC 2.4.1.5)
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FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAU OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

CAPALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N) =

D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).

D-FRUCTONE + (1,6-ALPHA-D-GLUCOSYL)(N+1).
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SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES
BINDING PROTEIN FROM S.MUTANS.
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"Molecular analyses of
Streptococcus mutans.";
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STRAIN-MT4239, MT4245,
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Honda O., Kato C., Kuramitsu H.K.;
"Nucleotide sequence of the Streptococcus
the glucosyltransferase S enzyme.";
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ween the Swiss Institute. There are no way European Bioinformatics Institute. There are no way is non-profit institutions as long as its content is in no way lifted and this statement is not removed. Usage by and for commercial lifted and this statement is not removed. Usage by and for commercial lifted and this statement is not removed. How www.isb-sib.ch/announce/
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CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N) -
D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).
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Pred. No. 0.00044;
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GLUCAN-BINDING (APPROXIMATE).
4.5 X TANDEM REPEATS.
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167296B5A2E8C476 CRC64;
                                                                                                                       ght. It is produced through Bioinformatics and the EM
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InterPro; IPR003318; Clyco_hydro_70.
Pfam; PF01473; CW_binding_1; 11.
Pfam; PF02324; Glyco_hydro_70; 1.
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.; D88653; BAA26103.1; -.
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.; D88659; BAA26111.1; -.
.; D88662; BAA26115.1; -.
.; D89979; BAA26121.1; -.
ANDHLSILEAWSDNDTPYLHD
                 15; Conservative
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                                                                                                                  KKKYTO, -> EKEYTL (IN STRAIN MT4251).

A -> S (IN STRAIN MT4239),

TDOGSEA -> ADKGNDS (IN STRAIN MT4239 AND
MT4245).

TDOGS -> ADKGN (IN STRAINS MT4239 AND
MT4245).

E -> K (IN STRAIN MT4251).

E -> K (IN STRAIN MT4251).

G -> IR (IN STRAIN MT4251).

G -> R (IN STRAIN MT4245).

G -> R (IN STRAIN MT4245).

G -> R (IN STRAIN MT4239) MT4245,

MT4251, MT4467 AND MT8148).

S -> N (IN STRAIN MT4239).

Y -> C (IN STRAIN MT425).

S -> N (IN STRAIN MT425).

S -> L (IN STRAIN MT425).

O -> P (IN STRAIN MT4467).

O -> P (IN STRAIN MT4245).

N -> D (IN STRAIN MT4245).

N -> D (IN STRAIN MT4245).

N -> D (IN STRAIN MT4245).

N -> G (IN STRAIN MT4239, MT4245, MT4251.
21
                 1;
               Score 75; DB
Pred. No. 0.00
1; Mismatches
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D -> N (
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S -> A (IN : AND MT8148)
                                                                    AND MT8148).

R -> G (IN STRAINS MT4239, MT4245, MT4251, MT4467 AND MT8148).

R -> K (IN STRAIN MT4467).

RYYDKNSGNMYYNKYTLÂNGRRIGIDRWGIARYY
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MT4467).
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Q -> H (
D -> N (
E -> K (
V -> F (
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3 x 63 AA APPROXIMATE TANDEM REPEATS.
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2.
3.
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5C6541F0DCB0DF00 CRC64
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N STRAIN MT4239).
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0.0014;
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1 AND MT8148).
9 AND MT4245).
9, MT4245 AND
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                Gaps
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RESULT 7
G3PC_LEIME
ID G3PC_LEIME
AC 001558;
DT 01-FBB-1994
DT 15-JUL-1999
DE GLYCERALDEHYI
DE GAPCH
OS Leishmania mu
OC Eukaryota; BE
OX NCBI_TaxID=51
RN [1]
RN SEQUENCE FROM
RC STRAIN=SSP. II
RN Michels P.A. I.
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UL16_EBV STAN
P03221;
21-JUL-1986 (Rel. 0
21-JUL-1986 (Rel. 0
15-DEC-1998 (Rel. 3
BGLF2 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                        _EBV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00044; gpdh; 1.
PRINTS; PR00078; G3PDHDRGNASE
PROSITE; PS00071; GAPDH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, X65220; CAA46323.1; -.
PIR; S25142; S25142.
PIR; B48445; B48445.
HSSP; P06977; 1GAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular analysis of the cytosolic and glycosomal glyphosphate dehydrogenase in Leishmania mexicana.";
Mol. Blochem. Parasitol. 55:115-126(1992)

-i- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
STRAIN=SSP. MEXICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLYCERALDEHYDE
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15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=SSP. MEXICANA;
MEDLINE=93063042; Pub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=5665;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000173; GAP_DH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: CYTOPLASMIC. SIMILARITY: BELONGS TO THE GLYCERALDEHYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 + NAD(+) = 1,3-DIPHOSPHATEGLYCERATE + NADH
PATHWAY: FIRST STEP IN THE SECOND PHASE OF
SUBUNIT: HOMOTETRAMER.
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330 p
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(Rel. 38, Last annotation update)
YDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
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Blaauw M., Kohl L...
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175
35511 MW;
                                                                                                              STANDARD;
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38,
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                                                                                                                                                                                                                           318
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                                                                                                                                                                                                                                                                                                           Score 57; DB
Pred. No. 0.15
2; Mismatches
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GLYCERALDEHYDE 3-PHCSPHATE.
ACTIVATES THIOL GPOUP DURING; ED4B6D8E8A207F1E CRC64;
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MBL outstation -
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GSPC_TRYB
ID G3PC_T
AC P10097
AC P10097
DT 01-MAR
DT 01-MAR
DT 15-JUL
DE (GAPDH
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J. Gen.
-!- SIMI
                                                           MEDLINE-91640000, ... MAIL MICHAELS F.A.M., MARCHAND M., Kohl L., All Opperdoes F.R.;
"The cytosolic and glycosomal isoenzymes the cytosolic and glycosoma brucei have
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MEDLINE=92113548; PubMed=1662696;
Chen M.R., Hsu T.Y., Lin S.W., Chen J.Y., Yang C.S.,
Chen M.R., Hsu T.Y., Lin S.W., Chen J.Y., Yang C.S.,
"Cloning and characterization of cDNA clones corresponding
"Cloning and characterization of the Epstein-Barr vi)
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Gibson T.J., Hatfull G.,
Tuffnell P.S., Barrell B.
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EMBL; V01555; CAA24831.1; --
EMBL; S77132; AAB21113.1; --
PIR; A03784; QQBE40.
PIR; S33036; S33036.
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-i- SIMILARITY: BELONGS TO FAMILY THAT HSV-6 ORF11R, EHV-1 46, HCMV UL94,
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Gammaherpesvirinae; Lymp
CBI_TaxID=10377;
                                           dehydrogenase in Trypanosoma
relationship.";
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Eukaryota; Euglenozoa;
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EBV BDLF2, AND VZV 44
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                                                                of glyceraldehyde-3-phosphate a distant evolutionary
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CONFLICT
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MEDLINE-97197982; PubMed-9046098;

van Dyck L., Tettelin H., Purnelli

"An 18.3 kb DNA fragment from year
                                                                                                                      YGRI20C OR 66324.
Saccharomyces cerevisiae (Baker's yeast).
Saccharomyces Funqi; Ascomycota; Saccharomycotina; Saccharomyces:
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                  unknown open reading frames, of Ty and three tRNA genes."; Yeast 13:171-176(1997).
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PRINTS; PR00078; G3PDHDRGNASE.
PROSITE; PS00071; GAPDH; 1.
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. J. Biochem. 162:501-507(1987).
CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: CYTOPLASMIC. SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg White O., Hickey E.K., Peterson J., Utterback T., Berry Linher K., Weidman J., Khouri H., Craven B., Bowman C., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Eisen J., Fraser C.M.;
                                                                                                                                                                                           Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWLO29 from USA.";
Nucleic Acids Res. 28:2311-2314(2000).
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Kalman S., Mitchell W., Marathe R., Lammel C., Fan on
Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
"Comparative genomes of Chlamydia pneumoniae and C."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydia pneumoniae (Chlamydophila pneumoniae)
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydo
                                                                                                                                                                                                                                                                                                                                            MEDLINE=20330349; PubMed=10871362;
                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequences of Chlamydia trachomatis pneumoniae AR39."; Nucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-CWL029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein. SEQUENCE 275 AA; 3
                                                                                                                                                                                                                                                                                                                                                                             STRAIN-J138
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-AR39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=83558;
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                                                                    + NAD(+) = 1,3-DIPHOSPHATEGLYCERATE + NADH.
PATHWAY: FIRST STEP IN THE SECOND PHASE OF
SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC.
SIMILARITY: BELONGS TO THE GLYCERALDEHYDE :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      European
                                                  DEHYDROGENASE FAMILY.
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; z72905; CAA97130.1;
s0003352; SEC35.
SWISS-PROT entry is copyright.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               non-
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Pred. No. 6.1;
6; Mismatches
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5.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.2.1.12) (GAPDH).
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                                                                                                                                                GLYCOLYSIS
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y K., Bass
, Dodson R.
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PCHA_PSEAE
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Best Local S
Matches
                                                                                                       SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed=10984043;
MEDLINE-20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou
Garber R.L., Goltry L., Tolentino E., Westbrock-Waddman S., Yuan Y.
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Smith K.A., Spencer D.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                           PCHA_PSEAE
Q51508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between
the Euro
                                                                                                                                                                                                                                Mol.
                                                                                                                                                                                                                                           STRAIN=ATCC 15692 / PAO1;
MEDLINE=96085939; PubMed=7500944;
Serino L., Reimmann C., Baur H., |
"Structural genes for salicylate |
Pseudomonas aeruginosa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                  "Complete genome sequence of Pseudomonas aeruginosa opportunistic pathogen.";
                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
SALICYLATE BIOSYNTHESIS ISOCHORISMATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycolysis;
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PRINTS; PR00078; G3PDHDRGNASE
PROSITE; PS00071; GAPDH; 1.
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                                                                        Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa
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SIMILARITY: STRONG, TRPE AND PABB.
                     (PROBABLE).
CATALYTIC ACTIVITY:
PATHWAY: SALICYLATE
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151 151 GLYCERALDEHYDE 3-PHOSPHATE
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                                   ACTIVITY: CHORISMATE = ISOCHORISMATE
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ACTIVATES THIOL
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Mismatches
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biosynthesis
           ISOCHORISMATE SYNTHASES;
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SYNTHASE
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7.7;
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GAMT_HUMAN
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Q14353;
Q14NV-1997 (Rel. 35, Created)
Q1-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CHANTOINOACETATE N-METHYLTRANSFERASE (EC 2.1.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isbrandt D., von Figura K.;
"Cloning and sequence analysis
methyltransferase cDNA.";
                         Kronmiller B., Arellano A., Montgomery M., Ow Kobayashi A., Olsen A.S., Carrano A.V.; Submitted (JUL-1998) to the EMBL/GenBank/DDBJ
                                                                                                   SEQUENCE FROM N.A.

Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwage
Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwage
Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
Danganan L., Poundstone P., Christensen M., Georgescu A., Avi
Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,
Coeffeld J., Duarte S., Lucas S., Bruce R., Thomas P., Quan (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The human guanidinoacetate methyltransferase (GAMT) syntenic region on 19p13.3, homologous to band C of r 10, but GAMT is not mutated in jittery stoe.", Biochem. Biophys. Res. Commun. 238:723-727(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X82644; CAA57969.1; -. EMBL; AE004840; AAG07619.1;
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Isbrandt D., Schmidt A.;
"Gene structure of human
Submitted (SEP-1999) to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochim. Biophys. Acta 1264:265:267(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAMT_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97472276; PubMed=9325156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-9606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jenne
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  CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e D.E., Olsen A.S., Zimmer M.;
human guanidinoacetate methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DHLSILEAWSDNDTPYLH
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Primates;
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the EMBL/GenBank/DDBJ databases S-ADENOSYL-L-METHIONINE + GUANI
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the EMBL/GenBank/DDBJ databases.
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Pred.
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                                                                                                           Quan G.,
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                                                                                                                                                                 Avila
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Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Last sequence update)
PUTATIVE ENDOCLUCANASE TYPE F PRECURSOR (EC 3
GLUCANASE) (CELLULASE).
FUSATIUM CXVSCOCYMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GUNF_FUSOX P46239;
                                                                                                                                                                                                         cellulase homologue cDNAs from Fusarium oxysporum.";
Gene 150:163-167(1994).
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-GLUCOSIDIC
                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel.
01-NOV-1995 (Rel.
01-NOV-1995 (Rel.
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content
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                                       or send an
                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=95047531; PubMed=7959045; Sheppard P.O., Grant F.J., Oort F
                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomy
Hypocreales; mitosporic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                      "The use of conserved
                                                                                                                                                                     <del>-</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PATHWAY: LAST STEP OF CREATINE BIOSYNTHESIS.
DISEASE: DEFECTS IN GAMT ARE RESPONSIBLE FOR REUROLOGIC SYNDROMI AND MUSCULAR HYPOTONIA. BIOCHEMICALLY IT IS CHARACTERIZED BY LOW EXCRETION OF CREATINE, DEFICIENCY OF CREATINE AND CREATINE ENOUGHATE, AND SIMULTANEOUS ACCUMULATION OF GUANIDINOACETATE IN
                                                                                                                                                                  SIMILARITY: CONTAINS 1
SIMILARITY: BELONGS TO
                                                                                                                                                      HYDROLASES).
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                                                                                                                                                                                               LINKAGES IN CELLULOSE
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                                                  non-profit institutions as long as its content is and this statement is not removed. Usage by and for requires a license agreement (See http://www.isb-sib.
                                       email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 AA;
                                                                                                                                                                                                                                                    O., Grant F.J., Oort P.J., Sprecher Opshall A., McKnight G.L., O'Hara P. conserved cellulase family-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Methyltransferase
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             AAA65588.1;
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                                                                                                                                                                                                                                                                                                                                                                   Ascomycota;
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                                                                                                                                                                   FUNGAL-TYPE CELLULOSE-BINDING CELLULASE FAMILY F (FAMILY 10
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MBL outstation -
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InterPro; IPR000254; CBD\_fungal.

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est Local Similarity
Matches 10; Conserv
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ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
XAA-PRO AMINOPEPTIDASE II (EC 3.4.11.9) (X-PRO AMINOPEPTIDASE II)
(AMINOPEPTIDASE P II) (APP) (PEPP II) (AMINOACYLPROLINE AMINOPEPTIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00562; CBD_FUNGAL; 1.
PROSITE; PS00591; GLYCOSYL_HYDROL_F10; 1.
Cellulose degradation; Hydrolase; Glycosi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00734; CBD_1; 1. Pfam; PF00331; G1yco_hydro_10; 1. PRINTS; PR00134; GLHYDRLASE10. ProDom; PD001821; CBD_fungal; 1. SMART; SM00236; fCBD; 1.
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                                                                                                                                                                                                                    SEQUENCE FROM N.A.

SPECTES=S.lividans; STRAIN=66;

MEDLINE=94176084; PubMed=7765336;

Butler M.J., Aphale J.S., Dizonno M.A., Krygsman P., Walczyk E.,

Malek L.T.;
                                                                                                                                                                                                                                                                                                           Oliver K., Harris D., Rajandream M.A.;
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. SPECIES=S.coelicolor; Oliver K., Harris D.,
                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces coelicolor, and Streptomyces lividans. Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMP2_STRCO
Q60394;
  entities
                                                                                                                                                                                                                                                                                               Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                         Actinomycetales;
NCBI_TaxID=1902,
                                                                                                                                                                                                                                                                                                                                                                                                                             PEPP2 OR SCG61.34C
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and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/
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1 19 POTENTIAL.
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Bentley S.D.,
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Pfam; PF00557; Peptidase_M24; 1.
PROSITE; PS00491; PROLINE_PEPTIDASE; 1.
Hydrolase; Aminopeptidase; Manganese; Zinc.
SEQUENCE 470 AA; 51924 MW; 0D3D33CEZ56523C2 CRC64;
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Fujiwara T., Terao Y., Hoshino T., Kawabata
Kimura S., Hamada S.;
"Molecular analyses of glucosyltransferase
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InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 9.
Pfam; PF02324; Glyco_hydro_70; 1.
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FEMS Microbiol. Lett. 161:331-336(1998).
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            FEMS Microbiol. Lett. 161:331-336(19 EMBL; D89978; BAA26120.1; -. InterPro; IPR002479; CW_binding. InterPro; IPR003318; Glyco_hydro_70. Pfam; PF01473; CW_binding_1; 9. Pf0m; PF02324; Glyco_hydro_70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kimura S., Hamada S.;
"Molecular analyses of glucosyltransferase
Streptococcus mutans.";
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Pfam; PF02324; Transferase.
                                                                                                                                     Streptococcus mutans."
                                                                                                                                                                                                                                        STRAIN-MT4467;
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NCBI_TaxID=1309;
                                                                                                                                                                                                                                                                                                                                                       Streptococcus mutans
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Fujiwara T., Terac
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"Molecular analyses of
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Q59983;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Q1UCOSYLTRANSFERASE-I PRECURSOR (EC 2.4.1.5) (DEXTRANSUCRASE) (SUCROSE
      MEDLINE=94146405; PubMed=8312602;
Sato S., Inoue M., Handa N., Alzawa Y., Isobe Y., Katayama T.;
"DNA sequence of the glucosyltransferase gene of serotype d
Streptococcus sobrinus.";
DNA seq. 4:19-27(1993).
-1- CATALYTIC ACTIVITY: SUCROSE + ((1,6)-ALPHA-D-GLUCOSYL)(N)
FRUCTOSE + ((1,6)-ALPHA-D-GLUCOSYL)(N+1).
EMBL; D13858; BAA02976.1; -...
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EMBL; D63570; BAA09792.1; -
InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_bydro_70.
Pfam; PF01473; CW_binding_1; 15.
Pfam; PF012324; Glyco_bydro_70; 1.
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                                                                                   SEQUENCE FROM N.A. STRAIN=OMZ176;
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NCBI_TaxID=1310;
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SEQUENCE 1590 AA;
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pfam; PF01473; CW_binding_1; 16.
pfam; PF02324; Glyco_hydro_70; 1.
Signal; Transferase; Glycos/transferase.
SIGNAL 1 38 POTENTIAL.
CHAIN 39 1590 GLUCOSYLTRANSFERASE-I.
EQUENCE 1590 AA; 175955 MW; C3C83A57CF3C2B0E C
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SEQUENCE FROM N.A.
STRAIN=NRRL B-512F;
                                                                                                                                                            Leuconostoc mesenteroides.
Bacteria; Firmicutes; Bacillus/Clostridium
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InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 10.
Pfam; PF02324; Glyco_hydro_70; 1.
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Pred. No. 0.00
1; Mismatches
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Pred. No. 4.5e-08;
3; Mismatches 0
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                                                                                                                                                                Lactobacillaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro: IPR002479; CW_binding.
InterPro: IPR00318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 14.
Pfam; PF02324; Glyco_hydro_70; 1.
Transferase; Glycosyltransferase.
SEQUENCE 1477 AA; 164886 MW; E6F
                                                                                                                                                                                                                                                       01-JUN-1998 (TremBLrel. 06, Created)
01-JUN-1998 (TremBLrel. 06, Last sequence update)
01-JUN-2001 (TremBLrel. 17, Last annotation update)
GLUCOSYLTRANSFERASE (EC 2.4.1.5) (DEXTRANSFORASE) (SUCROSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence analysis of the gene encoding alternansucrase, a sucrose glucosyltransferase from Leuconostoc mesenteroides NRRL B-1355."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AJ250172; CAB76565.1; -
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                                                                                                              Leuconostoc mesenteroides.
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
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Bacteria; Firmicutes; Bac
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01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-CUV-2001 (TrEMBLrel. 17, Last annotation update)
DEXTRANSUCRASE (EC 2.4.1.5).
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GLUCOSYLTRANSFERASE.
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Q9EZH5;
01-MAR-2001
                                                                                                                                                                                        Q9LCH3;
                       Streptococcus oralis.
Bacteria, Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kim H.-S., Kim D., Ryu H.-J., Robyt J.F.;
"Leuconostoc mensenteroides B-742CB, a dextransucrase gene.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF294469; AAG38021.1;
-InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 14.
Pfam; PF01473; CW_binding_1; 14.
SEQUENCE 1508 AA; 168542 MW; E2FCFA0F87AE4F3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monchois V., Remaud-Simeon M., Monsan P., Willemot R.M.;
FEMS Microbiol. Lett. 0:0-0(1998).
-!- GATALYTIC ACTIVITY: SUCROSE + ((1,6)-ALPHA-D-GLUCOSYL)(N) -
ENUCTOSE + ((1,6)-ALPHA-D-GLUCOSYL)(N+1).
EMBL; AF030129; AAB95453.1;
-InterPro; IPR002349; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF00473; CW_binding_1; 14.
Pfam; PF00473; CW_binding_1; 14.
Transferase; Glycosyltransferase.
SEQUENCE 1508 AA; 168511 MW; E70CECB57A70D1F0 CRC64;.
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DEXTRANSUCRASE DSRB742.
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STRAIN-NRRL B-1299;
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Infect. Immun. 68:2475-2483(2000).
EMBL; AB025228; BAA95201.1;
InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PP01473; CW_binding_1; 17.
Pfam; PP02324; Glyco_hydro_70; 1.
Transferase.
SEQUENCE
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Q54178;
                                                                                                                                                                                                    MEDLINE=92276337; PubMed=1534326; Sulavik M.C., Tardif G., Clewell D.B.; Sulavik M.C., Tardif G., Clewell D.B.; "Identification of a gene, rgg, which regulates expression of glucosyltransferase and influences the Spp phenotype of Streptococcus gordoni Challis."; "J. Bacteriol. 174:3577-3586(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus gordonii challis.
Bactaria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                    InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 18.
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EMBL; U12643; AAC43483.1; -.
EMBL; M89776; AAA26969.1; -.
                                                                                                                                                                                                                                                                              SEQUENCE OF 1-96 FROM N.A. STRAIN-CHALLIS;
                                                                                                                                                                                                                                                                                                                                MEDLINE=96157084; PubMed=8586195;
Vickerman M.M., Sulavik M.C., Clewell D.B.;
"MoLecular analysis of Streptococcus gordon
phase variants.";
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MEDLINE-20231779; PubMed-10768934;
Fujiwara T., Hoshino T., Ooshina T.,
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=CHALLIS;
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InterPro; IPR003318; Glyco.hydro_70.
Pfam; PF01473; CW_binding_1; 16.
Pfam; PF02324; Glyco.hydro_70; 1.
SEQUENCE 1527 AA; 169709 MW; 1DF
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=NRRL B-512-F;
Bhatnagar R., Singh D.K.S.;
                                                                                                                                                                                                 "Cloning and Molecular Characterization of Dextransucrase Leuconostoc mesenteroides NRRL B-512F.";
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U81374; AAD10952.1; -
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Bacteria; Firmicutes; Bac
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4: /cgn2_6/ptodata/2/paa/US099_COMB.pep: *
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Copyright (c) 1993 - 2000 Compugen Ltd
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/cgn2_6/ptcdata/2/paa/US07_COMB.pep:*
/cgn2_6/ptcdata/2/paa/US08_COMB.pep:*
/cgn2_6/ptcdata/2/paa/US082_COMB.pep:*
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 US-09-757-848-2

US-09-740-274-2

US-09-720-049-15

US-09-290-049-17

US-09-290-049-17

US-09-290-049-2

US-09-290-049-18

US-09-290-049-18

US-09-290-049-18
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4.629 Million cell updates/sec
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Sequence 2, Appli
Sequence 15, Appli
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Sequence 4, Appli
Sequence 17, Appli
Sequence 2, Appli
Sequence 19, Appl
Sequence 18, Appli
Sequence 2, Appli
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US-09-955-732-15	-09-775-925-	-60-212-413	764-903	764-854	-01358	1-01	4-109	75-925	-14827	63-233	-60-163-233-	-09-417-507-4294	-09-489-0	-08-951-7	-09-268-3	-09-268-3	-09-268-3	09-107-532	-09-107-5	-09-540-236-	-09-764-89	US01-013:	-09-107-532	09-107-53	-US99-22853	99-2	-US99-22853B-186	-09-517	-09-417-507-2450	-417-507-2645	-09-816-660-198	US-09-733-089-19824	US-09-740-274-6	5	-09-290-049
15,	equence	e 234	e 1513	е 362,	362,	Sequence 1513, Ap	23423,	e 31, 7	8870, 1	3947,	3282,	4	_	ω	4	Sequence 46, Appl	38,	4217,	4217,	2983	5098	3098, z	Sequence 7020, Ap	e 7020,	1863,	equence 1864,	1865,	449, Ap	e 24503,	Sequence 26458, A	Sequence 19824, A	198	9	e 2,	Sequence 16, Appl

## ALIGNMENTS

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RESULT 1
US-09-557-848-2
US-09-557-848-2
Sequence 2, Application US/09557848
GENERAL INFORMATION:
APPLICATE: NICHOLS, Scott E.
TITLE OF INVENTION: Substitutes for Modified Starch and
TITLE OF INVENTION: Latexes in Paper Manufacture
FILIR REPERENCE: 0356D2
CURRENT PAPLICATION NUMBER: US/09/557,848
CURRENT FILING DATE: 12000-04-26
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 09/007,999
EARLIER FILING DATE: 1995-06-07
EARLIER FILING DATE: 1998-01-16
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1475
TYPE: PAT
ORGANISM: Streptococcus mutans
US-09-557-848-2

Query Match
100.0%; Score 95; DB 19; Length 1475;
Best Local Similarity 100.0%; Pred. No. 4 5e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps
Oy
1 VPSYSFIRAHDSEVQDLIA 19
US-09-552 VPSYSFIRAHDSEVQDLIA 570
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APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, Martin A.
APPLICANT: Taubman, Martin A.
APPLICANT: Taubman, Martin A.
APPLICANT: Taubman, Martin A.
APPLICANTON: CARIES
FILE REFERENCE: FDC98-01p2A
CURRENT APPLICATION NUMBER: US/09/290,049
CURRENT FILING DATE: 1999-04-12
EARLIER APPLICATION NUMBER: 60/081,550
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-01-08
EARLIER APPLICATION NUMBER: 60/115,142
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                                                                                                                                                                                                                                                                                                                                                                                                                   ; SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 15
; LENGTH: 22
; TYPE: PRT
; ORGANISM: S. mutans
US-09-290-049-15
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CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 09/210,361
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: 09/007,999
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 08/478,704
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 09/009,620
PRIOR APPLICATION NUMBER: 09/009,620
PRIOR APPLICATION NUMBER: 09/009,620
PRIOR FILING DATE: 1998-01-20
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Best Local S
Matches 18
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LENGTH: 1475
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Best Local :
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PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 08/482,711
PRIOR FILING DATE: 1995-06-07
NUMBER OF THE PRIOR PR
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TITLE OF INVENTION: Glucan-containing Compositions and Paper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
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                                                                                               1 VPSYSFIRAHDSEVQDLI 18
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FILING DATE: 1995-06-07
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Similarity 100.0%;
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100.0%; Pr
0;
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; Pred. No. 1.3
0; Mismatches
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Pred. No.
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hes 0;
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Best Local S
Matches 18
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 17
LENGTH: 22
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Best Local Similarity
Matches 17; Conser
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                                                                                                                                                                                                                                                                      FILE REFERENCE: FDC98-01p2A
CURRENT FILLING DATE: 199-04-12
CURRENT FILLING DATE: 1999-04-12
EARLIER APPLICATION NUMBER: 60/081,550
EARLIER FILLING DATE: 1998-04-13
EARLIER FILLING DATE: 1998-01-08
EARLIER FILLING DATE: 1999-01-08
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1998-01-20
PRIOR APPLICATION NUMBER: 08/485,243
PRIOR FILING DATE: 1995-06-07
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PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 08/478,704
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 09/009,620
PRIOR FILING DATE: 1998-01-20
PRIOR FILING DATE: 1998-01-20
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CURRENT FILING DATE: 2000-12-19
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PRIOR APPLICATION NUMBER: 09/U
PRIOR APPLICATION NUMBER: 09/U
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                                                                                                                                                                                       TYPE: PRT
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                   1 VPSYSFIRAHDSEVQDLI 18
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VPSYSFARAHDSEVQDLI 18
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                                                                  Conservative
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                                                                                  90.5%;
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                                                                  0;
                                                                                  Score
Pred.
                                                                  Mismatches
                                                                                  No.
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o. 2.1e-06;
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1e-07;
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RESULT 8
US-09-290-049-18
; Sequence 18, Application US/09290049
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; ORGANISM: S.
US-09-290-049-19
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Best Local Similarity
Matches 19; Conserv
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LENGTH: 20
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                                                                                                                                                                    Matches
                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, MATTLIN A.
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARIES
FILE REFERENCE: FDC98-01,02A
CURRENT APPLICATION NUMBER: US/09/290,049
CURRENT FILING DATE: 1999-04-12
EARLIER APPLICATION NUMBER: 60/081,550
EARLIER APPLICATION NUMBER: 60/115,142
EARLIER APPLICATION NUMBER: 60/115,142
EARLIER FILING DATE: 1998-04-04
EARLIER FILING DATE: 1999-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: FDC98-01p2A
CURRENT APPLICATION NUMBER: US/09/290,049
CURRENT FILING DATE: 1999-04-12
EARLIER APPLICATION NUMBER: 60/081,550
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-18
EARLIER FILING DATE: 1999-01-08
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APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: SYMPHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARIES
                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 3.0
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                  Local Similarity
les 16; Conserv
                                                                                             1 VPSYSFIRTAHDSEVQDLIA 20
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                                                                                                                                                                  Conservative
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95.0%;
                                                                                                                                                                                 88.4%;
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Pred. No. 1.6e
0; Mismatches
                                                                                                                                                                                 Score 84; L
Pred. No. 2.
                                                                                                                                                                  Mismatches
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0;
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                                                                                                                                                                                   3e-07;
                                                                                                                                                                  1; Indels
                                                                                                                                                                                                Length 22;
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US-09-290-049-16; Sequence 16, Application US/09290049; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/499,203
CURRENT FILING DATE: 2000-02-08
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09499203 GENERAL INFORMATION:
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LENGTH: 22
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Best Local Sin Larity 61.7
Matches 11. Conservative
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Best Local Similarity
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TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL

TITLE OF INVENTION: CARLES

FILE REFERENCE: FDC98-01p2A
CURRENT FILING DATE: 1999-04-12

EARLIER APPLICATION NUMBER: 60/081,550
EARLIER APPLICATION NUMBER: 60/081,550
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 19
NUMBER OF SEQ ID NOS: 19
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APPLICANT: Smith, Daniel J.
FILE REFERENCE: FDC98-01p2A CURRENT APPLICATION NUMBER: US/09/290, CURRENT FILING DATE: 1999-04-12 EARLIER APPLICATION NUMBER: 60/081,550 EARLIER FILING DATE: 1998-04-13
                                                                                              APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES
TITLE OF INVENTION: CARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KOSSMANN, Jens
APPLICANT: WELSH, Thomas
APPLICANT: QUANZ, Martin
APPLICANT: KNUTH, Karola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Nucleic Acid Molecules Encoding Alternansucrase FILE REFERENCE: 147-196P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2057
                                                                                                                                                                                                                                                                                                  757 IPNYSFVRAHDYDAQDPI 774
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61.1%;
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78.9%;
                                                          US/09/290,049
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Pred. No. 0.099;
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Pred. No.
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ches 3;
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: EARLIER APPLICATION NUMBER: 60/115,142
: EARLIER FILING DATE: 1999-01-08
: NUMBER OF SEQ ID NOS: 19
: SOFTWARE: FastSEQ for Windows Version 3.0
: SEQ ID NO 16
: SEQ ID NO 16
: LENGTH: 22
: TYPE: PRT
: ORGANISM: S. mutans
US-09-290-049-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LENGTH: 1430
TYPE: PRT
ORGANISM: Streptococcus mutans
US-09-649-885-2
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APPLICANT: Nichols
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Best Local Similarity 76.5
Matches 13; Conservative
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PRIOR ELLANGUATE: 08/4
PRIOR APPLICATION NUMBER: 08/4
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 09/0
PRIOR ETITING DATE: 1998-01-16
                                                                       PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 08/4
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 09/C
PRIOR FILING DATE: 1998-01-20
                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/740,274
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 09/210,361
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: 09/007,999
PRIOR APPLICATION NUMBER: 09/007,999
PRIOR FILING DATE: 1998-01-16
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PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 2
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CURRENT FILING DATE: 2000-08-28
PRIOR APPLICATION NUMBER: US 09/008,172
PRIOR FILING DATE: 1998-01-16
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                                                                                                                                                                                                                                                                                        APPLICANT: Nichols, Scott E.
TITLE OF INVENTION: Glucan-containing Compositions and Paper
                                                                                                                                                                                                                                                                          FILE REFERENCE:
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nes 13; Conserv
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UMBER: US 09/008,172
1998-01-16
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76.58;
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76.5%;
                                                           08/485,243
                       09/008,172
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Pred. No.
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Pred. No. 0.095;
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Query Match
Best Local Similarity
Watches 9; Conserve
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US-09-733-089-19824
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                                                                                                                                                                                                          Sequence 19824, Application US/09816660 GENERAL INFORMATION:
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SEQ ID NO 19824
LENGTH: 263
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SOFTWARE: FastSEQ fo
SEQ ID NO 6
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Best Local Similarity
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APPLICANT: Wu, Wei
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Transcription In Plants
FILE REFERENCE: 38-21(15300)D
CURRENT APPLICATION NUMBER: US/99/816,660
CURRENT FILING DATE: 2001-03-26
                                                                                                                                                     APPLICANT: Dotson, Stanton APPLICANT: Kovalic, David APPLICANT: Liu, Jingdong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 09/474,435
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: US 09/654,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Dotson, Stanton APPLICANT: Kovalic, David APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 09/620,392
PRIOR FILING DATE: 2000-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/733,089
CURRENT FILING DATE: 2000-12-11
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FILE REFERENCE: 38-21(15300)D
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576 NYIFIRAHDSEVQTVIA 592
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Lutfiyya, Linda L.
McIninch, James
                                                                                                                   Liu, Jingdong
Lutfiyya, Linda L.
McIninch, James
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76.58;
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45.0%;
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Pred. No. 6.
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Pred. No. 0.095;
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PRIOR APPLICATION NUMBER: US 09/474,435
PRIOR FILLING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: US 09/654,617
PRIOR APPLICATION NUMBER: US 09/654,617
PRIOR FILLING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 09/733,089
PRIOR RILLING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/684
PRIOR FILLING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 09/620,392
PRIOR FILLING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 24143
SEQ ID NO 19824
LENGTH: 263
TYPE: PRT
ORGANISM: Oryza sativa
US-09-816-660-19824
                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-09-417-507-26458
(Sequence 26458, Application US/09417507
(GENERAL INFORMATION:
APPLICANT: KEITH G. WEINSTOCK ET AL.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATH99-10
CURRENT APPLICATION NUMBER: US/09/417,507
CURRENT APPLICATION NUMBER: US/09/417,507
CURRENT FILING DATE: 1999-10-14
NUMBER OF SEQ ID NOS: 44312
SEQ ID NO 26458
LENGTH: 541
TYPE: PRT
ORGANISM: A.fumigatus
US-09-417-507-26458
Search completed: March 27, 2002, 14:20:23 Job time: 1570 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 52.1%; Score 49.5; DB 22; Best Local Similarity 45.0%; Pred. No. 6.7; Matches 9; Conservative 6; Mismatches 4;
                                                                                                                                                                                                                                    Query Match 49.5%; Score 47; DB 18; Length 541; Best Local Similarity 47.6%; Pred. No. 46; Matches 10; Conservative 4; Mismatches 5; Indels
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116 LPSFPYVRAHDNGEISDTAA 135
                                                                                                                          1 VPSYSFIRAHDSE--VQDLIA 19
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204 VPQHSFLAQHDQQASVQSLLA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Mismatches
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Run on:
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March 27, 2002, 14:22:45; Search time 137.48 Seconds (without alignments) 9.536 Million cell updates/sec
                                                                                                                                                                                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Title: Perfect score: US-09-290-049A-2 95 1 VPSYSFIRAHDSEVQDLIA 19

Sequence:

Scoring table: BLOSUM62

Searched:

Gapop 10.0 , Gapext 0.5

tal number of hits satisfying chosen parameters:

332938

332938 seqs, 68999538 residues

imum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pending\_Patents\_AA\_New:\*

1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:\*

7: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep:\*

8: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	s	4	ω	2	L	Result No.
40.5	40.5	40.5	41	44	47	65	65	65	66	66	67	73	73	80	84	84	84.5	86	86	91	91	95	95	95	Score
42.6	42.6	42.6	43.2	46.3	49.5	68.4	68.4	68.4	69.5	69.5	70.5	76.8	76.8	84.2	88.4	88.4	88.9	90.5	90.5	95.8	95.8	100.0	100.0	100.0	Query Match Length
414	398	389	633	327	274	545	22	22	1278	535	584	22	22	523	22	22	20	22	22	22	22	23	19	19	
9	σ	σ	σ	œ	σ	6	σ	σ	6	σ	6	σ	σ	σ	Φ	σ	0	σ	6	6	δ	σ	6	6	DB
US-09-708-427-10450	US-09-708-427-10451	US-09-708-427-10452	US-09-605-703B-440	US-60-356-051-2881	US-09-675-784A-9123	US-09-604-957-4	US-09-290-049A-16	US-09-562-328-29	US-09-604-957-3	US-09-604-957-7	US-09-604-957-6	US-09-290-049A-18	US-09-562-328-31	US-09-604-957-5	US-09-290-049A-19	US-09-562-328-32	US-09-562-328-26	US-09-290-049A-17	US-09-562-328-30	US-09-290-049A-15	US-09-562-328-28	US-09-562-328-44	US-09-290-049A-2	US-09-562-328-27	ID
Sequence 10450, A	Sequence 10451, A	10452	440, 2		913	Sequence 4, Appli	Sequence 16, Appl	29	ω	7,	6, 7	18,	31,	5, b	19,	•	Sequence 26, Appl		30,		Sequence 28, Appl	Sequence 44, Appl	Sequence 2, Appli	Sequence 27, Appl	Description

40 42.1 547 6 US-09-943-857-4 40 42.1 547 6 US-09-943-857-4 40 42.1 547 6 US-09-943-857-6 40 42.1 547 6 US-09-943-857-6 40 42.1 572 1 PCT-US02-03987-5626 40 42.1 572 1 US-09-815-242-5626 40 42.1 573 1 PCT-US02-03987-12247 40 42.1 573 1 PCT-US02-03987-12247 40 42.1 573 1 US-09-815-242-12247 40 42.1 573 6 US-09-815-242-12247 40 42.1 573 6 US-09-815-242-12247 40 42.1 573 7 US-10-072-851-12247 40 42.1 573 7 US-10-072-851-12291 40 42.1 573 7 US-10-072-851-12291 40 42.1 573 7 US-10-072-851-12291 40 42.1 573 6 US-09-708-427-2859 41 783 6 US-09-708-427-2859 41 1 309 6 US-09-675-784A-9068 39 41.1 309 6 US-09-675-784A-9068 39 41.1 309 6 US-09-675-784A-9068 41.1 309 6 US-09-675-784A-9068 41.1 309 6 US-09-675-784A-9068	42.1 547 6 0 42.1 547 6 0 42.1 547 6 0 42.1 572 1 0 42.1 572 7 0 42.1 573 1 0 42.1 573 1 0 42.1 573 6 0 42.1 573 7 0 42.1 573 7 0 42.1 573 7 0 42.1 573 7 0 42.1 737 6 0 42.1 737 6 0 42.1 737 6 0 42.1 737 6 0 42.1 737 6 0 42.1 737 6 0 42.1 737 6 0 42.1 737 6 0 42.1 737 6 0 42.1 737 6 0 42.1 737 6 0 42.1 738 6 0 42.1 738 6 0 42.1 738 6 0 42.1 739 6 0 42.1 730 6	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	0.0
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5 5 5 5 5 6 7 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8	6 US-09-943-857-2 6 US-09-943-857-4 6 US-09-943-857-6 6 US-09-943-857-6 6 US-09-943-857-6 6 US-09-943-857-6 7 US-09-943-857-6 8 Sequence 1 PCT-US02-03987-5626 6 US-09-815-242-5626 9 PCT-US02-03987-12247 8 Sequence 1 PCT-US02-03987-12921 9 Sequence 1 US-09-815-242-12247 9 Sequence 1 US-09-815-242-12247 9 Sequence 1 US-09-915-242-12247 9 Sequence 1 US-09-915-242-12247 9 Sequence 1 US-09-708-427-2851 9 Sequence 1 US-09-708-427-2859 9 Sequence 1 US-09-45-7-84A-9068 9 Sequence 1 US-09-45-7-738-1852	41.1	41.1	41.1	41.1	42.1	42.1	42.1	42.1	42.1	42.1	42.1	42.1	42.1	42.1	42.1	42.1	42.1	42.1	42.1	
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			US-09-345-473E-37	US-09-609-360C-37	US-09-675-784A-9068	US-09-708-427-2857	US-09-708-427-2858	US-09-708-427-2859	US-10-072-851-12921	US-10-072-851-12247	US-09-815-242-12921	US-09-815-242-12247	PCT-US02-03987-12921	PCT-US02-03987-12247	US-10-072-851-5626	US-09-815-242-5626	PCT-US02-03987-5626	US-09-943-857-6	US-09-943-857-4	US-09-943-857-2	

## ALIGNMENTS

OY 1 VPSYSFIRAHDSEVQDLIA 19	Query Match 100.0%; Score 95; DB 6; Length 19; Best Local Similarity 100.0%; Pred. No. 5.5e-10; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RESULT 1 US-09-562-328-27 Sequence 27, Application US/09562328 GENERAL INFORMATION: APPLICANT: LEES, ANDREW APPLICANT: TAUBMAN, MARTIN A. APPLICANT: TAUBMAN, MARTIN A. APPLICANT: SMITH, DANIEL J. TITLE OF INVENTION: COLUMGATE VACCINES FOR THE PREVENTION OF DENTAL CARIES FILE REFERENCE: 0495.0046-01 CURRENT APPLICATION NUMBER: US/09/562,328 CURRENT APPLICATION NUMBER: US/09/562,328 CURRENT FILING DATE: 2000-05-01 PRIOR APPLICATION NUMBER: 09/288,965 PRIOR FILING DATE: 199-04-09 NUMBER OF SEQ ID NOS: 44 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 27 LENGTH: 19 TYPE: PRT ORGANISM: Streptococcus sp.
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; ORGANISM: Streptococcus sp. US-09-562-328-28
                                                                                                                                                                                                                                                                                                                                                                 US-09-562-328-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Streptococcus sp
US-09-562-328-44
                                                    PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 28
LENGTH: 22
PRIOR THE 22
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PRIOR THE 22
                                                                                                                                                                                                                                                                                                                     Sequence 28, Application US/09562328 GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: LEES, ANDREW
APPLICANT: TAUBMAN, MARTIN A.
APPLICANT: SMITH, DANIEL J.
TITLE OF INVENTION: CONJUGATE VACCINES FOR THE PREVENTION OF DENTAL CARIES
FILE REFERENCE: 04995,0046-01
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Best Local Similarity
Matches 19; Conserv
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Best Local Similarity 100.0%;
Matches 19; Conservative 0;
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LENGTH: 19
                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/562,328
CURRENT FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 09/288,965
                                                                                                                                                                                                                     APPLICANT: LEES, ANDREW
APPLICANT: TAUBMAN, MARTIN A.
APPLICANT: SMITH, DANIEL J.
TITLE OF INVENTION: CONJUGATE VACCINES FOR THE PREVENTION OF DENTAL CARIES
FILE REFERENCE: 04995.0046-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/562,328
CURRENT FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 09/288,965
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 44
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                                       TYPE: PRT
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ORGANISM: Artificial Sequence
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100.0%; Pred. No. 5.5e-10;
vative 0; Mismatches 0;
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Pred. No.
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Query Match Best Local Similarity

95.8%;

Score 91; Pred. No.

DB 6; L 3.2e-09;

Length 22;

RESULT 7 US-09-290-049A-17

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Дd
                           QY
                                                                                                                                                ; LENGTH: 22
TYPE: PRT
; ORGANISM: Streptococcus sp.
US-09-562-328-30
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US-09-290-049A-15
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                                                       Query Match
Best Local Similarity
Matches 17; Conserv
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SOFTWARE: PatentIn Ver.
SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 15 LENGTH: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 30, Application US/09562328
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                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/56;
CURRENT FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 09/288,965
PRIOR FILING DATE: 1999-04-09
                                                                                                                                                                                                                                                                                                                                  APPLICANT: SMITH, DANIEL J.
TITLE OF INVENTION: CONJUGATE VACCINES FOR THE PREVENTION OF DENTAL CARIES FILE REFERENCE: 04995.0046-01
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LEES, ANDREW APPLICANT: TAUBMAN, MAI APPLICANT: SMITH, DANII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
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               1 VPSYSFIRAHDSEVQDLI 18
1 VPSYSFARAHDSEVQDLI 18
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                                                                Conservative
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Pred. No. 3.2
                                                              Score 86; DB 6;
Pred. No. 2.4e-08;
0; Mismatches 1
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Sequence 17, Application US/09290049A GENERAL INFORMATION:

APPLICANT: Smith, Daniel J APPLICANT: Taubman, Marti

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PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENCTH: 22
TYPE: PRT
ORGANISM: S. downei
US-09-290-049A-17
RESULT 5
US-09-562-328-32
Sequence 32, Application US/09562328
GENERAL INFORMATION:
APPLICANT: LEES, ANDREW
APPLICANT: TAUBMAN, MARTIN A.
APPLICANT: TAUBMAN, MARTIN A.
APPLICANT: SMITH, DANIEL J.
TITLE OF INVENTION: CONJUGATE VACCINES FOR THE PREVENTION OF DENTAL CARIES
FILE REFERENCE: 04995.0046-01
CURRENT APPLICATION NUMBER: US/09/562,328
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: SOFTWARE: Patentin Ver. 2.1
: SEO ID NO 26
: LENGTH: 20
: TYPE: PRT
: ORGANISM: Streptococcus sp.
09-562-328-26
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GENERAL INFORMATION:
APPLICANT: LEES, ANDREW
APPLICANT: TAUBMAN, MARTIN A.
APPLICANT: SMITH, DANIEL J.
APPLICANT: SMITH, DANIEL J.
TITLE OF INVENTION: CONJUGATE VACCINES FOR THE PREVENTION OF DENTAL CARIES
FILE REFERENCE: 04995,0046-01
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Best Local
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TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARLES
FILE REFERENCE: 1564.1008-002
CURRENT APPLICATION NUMBER: US/09/290,049A
CURRENT FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR FILING DATE: 1998-04-13
PRIOR FILING DATE: 1998-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/562,328
CURRENT FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 09/288,965
PRIOR FILING DATE: 1999-04-09
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les 19; Conserv
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les 17; Conserv
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Pred. No. 3.
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Pred. No. 2.4e-08;
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3.8e-08;
ches 0;
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US-09-290-049A-19
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US-09-290-049A-19
; Sequence 19, Application US/09290049A
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PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 19
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PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 32
                                                           SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 5
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                                                                                                   APPLICANT: RAHAOUI, HAKIM
APPLICANT: LEER, ROBERT-JAN
TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASE AND NOVEL GLUCAN
FILE REFERENCE: BO 43388
CURRENT APPLICATION NUMBER: US/09/604,957
CURRENT FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 00201871.1
PRIOR APPLICATION NUMBER: 00201871.1
PRIOR FILING DATE: 2000-05-25
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Best Local Similarity 88.9%;
Matches 16; Conservative
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CURRENT APPLICATION NUMBER: US/09/290,049A
CURRENT FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR FILING DATE: 1998-04-13
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TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARIES
                                                                                                                                                                                                                                                                                 APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA APPLICANT: DIJKHUIZEN, LUBBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Smith, Daniel APPLICANT: Taubman, Mar
                                                                                                 NUMBER OF SEQ ID NOS: 17
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TYPE: PRT
ORGANISM: Leuconostoc mesenteroides
                                    LENGTH: 523
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Pred. No. 5.
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Pred. No. 5
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US-09-604-957-5

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Sequence 31, Application US/09562328; GENERAL INFORMATION:
APPLICANT: LEES, ANDREW
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                                                                                                                                          ; ORGANISM: S. downei
US-09-290-049A-18
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US-09-290-049A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Streptococcus sp. US-09-562-328-31
                                                                                                                                                                        NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 18
SEQ ID NO 18
LENGTH: 22
TYPE: PRT
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SEQ ID NO 31
LENGTH: 22
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Best Local Similarity
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                                                                                      Query Match
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APPLICANT: SMITH, DANIEL J.
APPLICANT: SMITH, DANIEL J.
TITLE OF INVENTION: CONJUGATE VACCINES FOR THE PREVENTION OF DENTAL CARIES FILE REFERENCE: 04995.0046-01
CURRENT APPLICATION NUMBER: US/09/562,328
CURRENT FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 09/288,965
PRIOR APPLICATION NUMBER: 09/288,965
PRIOR APPLICATION NUMBER: 09/288,965
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                             APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARIES
FILE REFERENCE: 1564.1008-002
CURRENT APPLICATION NUMBER: US/09/290,049A
CURRENT FILING DATE: 1999-04-12
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                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/081,550 PRIOR FILING DATE: 1998-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                    equence 18, Application US/09290049A ENERAL INFORMATION: APPLICANT: Smith, Daniel J.
                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/115,142 PRIOR FILING DATE: 1999-01-08
                                            76.8%;
Local Similarity 78.9%;
les 15; Conservati...
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1 VPSYSFIRAHDSEVQDLIA 19
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78.9%;
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73.7%;
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Pred. No.
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Pred.
                                                                    Score 73; DB 6;
Pred. No. 4.1e-06;
                                                     Mismatches
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1.3e-05;
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SEQ ID NO 7
SEQ ID NO 7
LENGTH: 535
TYPE: PRT
ORGANISM: Lactobacillus reuteri
US-09-604-957-7
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                                                                  Query Match
Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/09604957

GENERAL INFORMATION:
APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
APPLICANT: DIJKHUIZEN, LUBBERT
APPLICANT: RAHAOUI, HAKIM
APPLICANT: LEER, ROBERT-JAN
TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASE AND NOVEL GLUCAN
FILE REFERENCE: BO 43388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 1:
SOFTWARE: PatentIn Ver.
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09604957 GENERAL INFORMATION:
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Best Local
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CURRENT FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 00201871.1
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/604,957
CURRENT FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 00201871.1
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
APPLICANT: DIJKHUIZEN, LUBBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASE AND NOVEL GLUCAN FILE REFERENCE: BO 43388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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167 IPNYSFVRAHDYDAQDPIS 185
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                                 1 VPSYSFIRAHDSEVODLI 18
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                                                                    Conservative
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Pred. No.
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. 0.0025;
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Search completed: March 27, 2002, 14:22:46 Job time: 1693 sec

Run on: OM protein - protein search, using sw model March 27, 2002, 14:01:15; Search time 102.51 Seconds (without alignments) 14.119 Million cell updates/sec GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

Title:
Perfect score:
Sequence: US-09-290-049A-2 95 1 VPSYSFIRAHDSEVQDLIA 19

Scoring table: BLOSUM62

219241 seqs, 76174552 residues Gapop 10.0 , Gapext 0.5

Searched:

stal number of hits satisfying chosen parameters: 219241

imum DB seq length: 0 aximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	σ	5	4	ω	2	1	Result
41	41	41	41.5	41.5	42	42	42	42	42	42	42	43	43	43	44	46	61	64	65	65	65	65	73	79	80	84	91	95	Score
43.2	43.2	43.2	43.7	43.7	44.2	44.2	44.2	44.2	44.2	44.2	44.2	45.3		45.3	9	8	64.2	67.4		68.4	68.4	68.4	76.8	٠	84.2	æ	95.8	100.0	Query Match
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DNA polymerase III			lysine decarboxyla	lysine decarboxyla	probable histone t	ribonuclease T2 ho	RNase II, mRNA deg	exoribonuclease II		probable D-lactate	crtX protein - Erw	protein F14D16.3 (	regulatory protein	hypothetical prote	probable RING zinc	intermediate filam	glucosyltransferas	glucosyltransferas	glucosyltransferas	glucosyltransferas	m .	dextransucrase (EC	OD.	dextransucrase (EC	probable dextransu	œ.	ansucras	fB protein pre	Description

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41.1	41.6	42.1	42.1	42.1	42.1	42.1	42.1	42.1	42.1	42.1	42.1	42.1	42.6	43.2
145	145	6359	1029	895	783	572	549	549	548	534	431	359	414	1146
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s07957	UCEEPP H84174	T31679	F86359	A86410	T00782	B28474	JN0551	JN0552	S32615	S41735	B37802	G82197	T06120	E70204
hypothetical prote	hypothetical prote	bacitracin synthet	hypothetical prote	protein F3M18.22 [	probable anthranil	phosphotransferase	triacylglycerol li	triacylglycerol li	triacylglycerol li	cholesterol estera	crtX protein - Erw	RstA1/RstA2 protei	hypothetical prote	hypothetical prote

## ALIGNMENTS

RESULT 2 JT0345 dextransucrase (EC 2.4.1.5) precursor - Streptococcus mutans (strain GS-5) N;Alternate names: sucrose 6-glucosyltransferase C;Species: Streptococcus mutans C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 24-Sep-1999 C;Accession: JT0345; C33135 R;Jedda, S; Shiroza, T; Kuramitsu, H.K. Gene 69, 101-109, 1988 A;Title: Sequence analysis of the gtfC gene from Streptococcus mutans GS-5. A;Reference number: JT0345; MUID:89137980 A;Accession: JT0345	Query Match Query Match Query Match Query Match Best Local Similarity 100.0%; Pred. No. 1.1e-07; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 VPSYSTRAHDSEVQDLIA 19 Db 552 VPSYSFIRAHDSEVQDLIA 570	0,	SULT 1 3135 3136 Brotein precursor - Streptococcus mutans Species: Streptococcus mutans Shiroza, T.; Ueda, S.; Kuramitsu, H.K. Bacteriol. 169, 4263-4270, 1987 Milecule type: DNA Residues: 1-1475 <shi-> Status: preliminary Molecule type: DNA Residues: 1-1475 <shi-> Status: preliminary Molecule type: DNA Residues: 1-1475 <shi-> Sibiroza, T.; Ueda, S.; Kuramitsu, H.K. Banitted to the Protein Sequence Database, September 1990 Recession: A33128 Status: preliminary: not compared with conceptual translation Molecule type: DNA Residues: 1-171,173-641, N.,663-1475 <sh2> Experimental source: strain GS-5 Superimental source: strain GS-5 Superimental source: strain GS-5 Superimental source: strain GS-5 Superimental source: prepeat homology <cp2> 1224-124-JChomain: cpl repeat homology <cp3> 1324-137-JChomain: cpl repeat homology <cp3> 134-137-JChomain: cpl repeat homology <cp3> 1354-137-JChomain: cpl repeat homology <cp3> 1364-137-JChomain: cpl repea</cp3></cp3></cp3></cp3></cp3></cp3></cp3></cp3></cp3></cp3></cp3></cp3></cp3></cp3></cp3></cp3></cp3></cp3></cp3></cp3></cp3></cp3></cp3></cp2></sh2></shi-></shi-></shi->
Query Match 100.0%; Score 95; DB 2; Length 1475; Best Local Similarity 100.0%; Pred. No. 1.1e-07; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 1 VPSYSFIRAHDSEVQDLIA 19 1			Molecule type: DNA; Molecule type: DNA; Residues: 1-171,173-641, 'N',643-1475 Experimental source: strain GS-5; Experfamily: cpl repeat homology; 1096-1115/Domain: cpl repeat homology; 1224-1243/Domain: cpl repeat homology; 1289-1308/Domain: cpl repeat homology; 1354-1373/Domain: cpl repeat homology; 1354-1373/Domain: cpl repeat homology; 1419-1438/Domain: cpl repeat homology
Molecule type: DMA  Residues: 1-171,173-641,'N',643-1475 <sh2>  Experimental source: strain GS-5  Superfamily: cpl repeat homology <cp1> 1096-111s/Domain: cpl repeat homology <cp2> 1224-1243/Domain: cpl repeat homology <cp3> 1289-1308/Domain: cpl repeat homology <cp4> 1354-1373/Domain: cpl repeat homology <cp5> 1419-1438/Domain: cpl repeat homology <cp5>  Query Match  100.0%; Score 95; DB 2; Length 1475;  Best Local Similarity 100.0%; Pred. No. 1.1e-07;  Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps  1 VPSYSFIRAHDSEVQDLIA 19                                       </cp5></cp5></cp4></cp3></cp2></cp1></sh2>	Residues: 1-171.173-641, 'N',643-1475 ;Residues: 1-171.173-641, 'N',643-1475 ;Experimental source: strain GS-5 ;Superfamily: cpl repeat homology ;1096-1115/Domain: cpl repeat homology ;1224-1243/Domain: cpl repeat homology ;1289-1308/Domain: cpl repeat homology ;1354-1373/Domain: cpl repeat homology ;1354-1373/Domain: cpl repeat homology ;1419-1438/Domain: cpl repeat homology		3639; PIDN:AAA88588.1; K. base, September 1990 th conceptual translati
Molecule type: DNA Cross-references: GB:M17361; NID:g153639; PIDN:AAA88588.1; PID:g153640 Shiroza, T.; Ueda, S.; Kuramitsu, H.K. bmitted to the Protein Sequence Database, September 1990 Reference number: A33128 Accession: A33128 Status: preliminary; not compared with conceptual translation Molecule type: DNA Signerimental source: strain GS-5 Experimental source: strain GS-5 Experimental source: strain GS-5 Superfamily: cpl repeat homology <cp1> 1224-1243/Domain: cpl repeat homology <cp2> 1384-1373/Domain: cpl repeat homology <cp3> 1384-1373/Domain: cpl repeat homology <cp3> 1419-1438/Domain: cpl repeat homology <cp5> Query Match  100.0%; Score 95; DB 2; Length 1475; Best Local Similarity 100.0%; Pred. No. 1.1e-07; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps  1 vPSYSFIRAHDSEVODLIA 19  11:1:1:1:1:1:1:1:1:1:1:1:1:1:1:1:1:1</cp5></cp3></cp3></cp2></cp1>	Molecule type: DNA ; Rosidues: 1-1475 <shl> ; Rosidues: 1-1475 <shl> ; Cross-references: GB:M17361; NID:g153639; PIDN:AAA88588.1; ; Cross-references: GB:M17361; NID:g153639; PIDN:AAA88588.1; ; Shiroza, T.; Ueda, S.; Kuramitsu, H.K.  Reference number: A33128 ; Reference number: A33128 ; Accession: A33128 ; Accession: A33128 ; Accession: A33128 ; Status: preliminary; not compared with conceptual translati ; Status: preliminary; not compared with conceptual translati ; Residues: 1-171,173-641,'N',643-1475 <sh2> ; Experimental source: strain GS-5 ; Superfamily: cpl repeat homology <cp1> ; 1284-1243/Domain: cpl repeat homology <cp2> ; 1289-1308/Domain: cpl repeat homology <cp3> ; 1284-1373/Domain: cpl repeat homology <cp4> ; 1419-1438/Domain: cpl repeat homology <cp5> ; 1419-1438/Domain: cpl repeat homology <cp5></cp5></cp5></cp4></cp3></cp2></cp1></sh2></shl></shl>		protein precursor - Streptococcus mutans scies: Streptococcus mutans scies: Streptococcus mutans energy of the protect of the graph of

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A;Reterence
A;Accession: A381/J
A:Status: preliminary
Olecule type: DNA
Cesidues: 1-1592 <ABO>
A;Cross-references: GB:D90213; NID:92
C;Superfamily: cpl repeat homology
F;1093-1112/Domain: cpl repeat homol
F;1222-1241/Domain: cpl repeat homol
F;1387-1306/Domain: cpl repeat homo
F;1330-1351/Domain: cpl repeat homo
F;1352-1371/Domain: cpl repeat homo
F;1402-1420/Domain: cpl repeat homo
F;1405-1484/Domain: cpl repeat homo
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A; Residues: 1-1375 <UED>
A; Experimental source: GS-5
R; Shiroza, T.; Ueda, S.; Kuramitsu, H.K.
J. Bacteriol. 169, 4263-4270, 1987
A; Title: Sequence analysis of the gtfB gene from Streptococcus mutans.
A; Reference number: A33135; MUID:87308013
A; Accession: C33135
probable dextransucrase (EC C; Species: Leuconostoc meser
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C;Species: Streptococcus sobrinus
C;Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 15-Oct-1999
C;Accession: A38175
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A;Molecule type: DNA
A;Residues: 1-349 <SHI>
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C;Function:
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Matches 16
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Pred. No. 8.7e-06;
1; Mismatches 1
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Pred. No.
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4.7e-07;
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                                                                                  Leuconostoc
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                                                                                       mesenteroides
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                                A; Molecule type: DN
Nonecidues: 1-1365
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C; Function:
A; Description:
C; Keywords: gly
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A; Residues: 1-1508 < MON>
A; Cross-references: EMBL: AF030129;
A; Cross-references: EMBL: AF030129;
R;Gilmore, K.S.; Russell, R.R.B.; Ferretti, J.J. Infect. Immun. 58, 2452-2458, 1990
A;Title: Analysis of the Streptococcus downei gtfs A;Reference number: A41483; MUID:90316665
A;Accession: A41483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 182, 23-32, 1996
A;Title: Cloning and sequencing of a gene A;Reference number: JC5473; MUID:97136686
A;Accession: JC5473
                                                                                                        glucosyltransferase (EC 2.4.1.-) gtfS precursor - SC:Species: Streptococcus sobrinus C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 C:Accession: A41483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Keywords: glycosyltransferase; hexosyltransferase F;78-870/Domain: catalytic **status predicted <CAT> F;922-1290/Domain: glucan-binding **status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-1290 <MON>
A; Residues: 1-1290 <MON>
C; Comment: This enzyme cataly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: JC5473
R;Monchois, V.; Willemot, R.M.; Remaud-Simeon, M.; Croux, C.; Monsan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Leuconostoc mesenteroides
C;Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 29-Aug-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Monchois, V.; Remaud-Simeon, M.; Monsan, P.; Willemot, FEMS Microbiol. Lett. 159, 307-315, 1998
A;Title: Cloning and sequencing of a gene coding for an & A;Reference number: Z20981; MUID:98164374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
C;Accession: T31098
                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: dsrA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: nucleic acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: dsrB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: T31098
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetics:
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                                                                                                                                                                                                                                                                                  388 PNYSFIRAHDSEVQTIIA
                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                   2 PSYSFIRAHDSEVQDLIA 19
|:||||||||||||
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                                                                                                                                                                                                                                                                                                                                                                l Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         enzyme catalyzes the transfer
                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.2%;
73.7%;
                                                                                                                                                                                                                                                                                                                                                                                      83.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           not shown; translation
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hexosyltransferase
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                  2;
                                                                                                                                                                                                                                                                                                                                                                                    Score 79; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NID:g2766611; PID:g2766612; PIDN:AAB95453.1
B-1299
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3.9e-05;
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                                                                                                                                                                                                                                                                                                                                                                                      .9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of D-glucopyranosyl units
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                                                                                                                                                                       Streptococcus sobrinus
                                             gene,
                                                                                                                              #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                          Length 1290;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <GCB>
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<GIL>

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F:181-201/Domain: cpl repeat homology <CP1>
F:1127-1146/Domain: cpl repeat homology <CP2>
F:1127-1127/Domain: cpl repeat homology <CP3>
F:1192-1211/Domain: cpl repeat homology <CP3>
F:1257-1276/Domain: cpl repeat homology <CP4>
F:1277-1297/Domain: cpl repeat homology <CP5>
F:1321-1340/Domain: cpl repeat homology <CP5>
F:1321-1340/Domain: cpl repeat homology <CP6>
F:13341-361/Domain: cpl repeat homology <CP6>
F:1341-361/Domain: cpl repeat homology <CP7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cession: A45866
nda, O.; Kato, C.; Kuramitsu, H.K.
J. Gen. Microbiol. 136, 2099-2105, 1990
A;Title: Nucleotide sequence of the Streptococcus mutans A;Reference number: A45866; MUID:91100958
A;Accession: A45866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M29296
C;Superfamily: cpl repeat homology
C;Keywords: 91ycosyltransferase; he
F;181-201/Domain: cpl repeat homol
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A45866
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                                                                                                                                                                                           A;Title: Streptococcus salivarius ATCC 25975 possesses A;Reference number: Z20909; MUID:95122197 A;Accession: T30857
                                                                                                                                                                                                                                                                                       glucosyltransferase - Streptococcus salivarius
C;Species: Streptococcus salivarius
C;Date: 22-Oct.1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C;Accession: T30857
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C;Superfamily: cpl repeat homolog
C;Keywords: glycosyltransferase;
                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-1449 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-1431 <HON>
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                                                                                                                 A;Cross-references: EMBL:L35495; NID:g662378; PID:g662379; PIDN:AAC41412.1
                                                                                                                                                                       A; Status: preliminary; translated
                                                                                                                                                                                                                                                     Infect. Immun. 63, 609-621, 1995
                                                                                                                                                                                                                                                                       R; Simpson, C.L.;
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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Best Local
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                                                                             gtfL
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15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                       Giffard, P.M.; Jacques, N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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76.5%;
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78.9%;
 68.4%;
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 Score
Pred.
                                                                                                                                                                         from GB/EMBL/DDBJ
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   No.
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 DB 2;
0.014;
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                 Length 1449;
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C; Accession: R; Jacques, N.
           glucosyltransferase (EC 2.4.1.-) S - Streptococcus salivarius
C;Species: Streptococcus salivarius
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: S22737; S28810; B44811; S22727
                                                                                         RESULT
S22737
                                                                                                                                                                                                                                                                                                                           C;Superfamily: cpl repeat homology
C;Keywords: glycosyltransferase; hexosyltransferase
F;1307-1326/Domain: cpl repeat homology <CP4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Giffard, P.M.; Simpson, C.L.; Milward, C.P.; Jacques, N.A. J. Gen. Microbiol. 137, 2577-2593, 1991
A;Title: Molecular characterization of a cluster of at least two A;Reference number: A44811; MUID:92148377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Streptococcus salivarius
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
C;Accession: A44811; S22726; S28809
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A44811
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C;Species: Streptococcus salivarius
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_ch
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A; Accession: A44811
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A; Residues: 1-1449 <JAF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, February 1998
A;Description: Streptococcus salivarius V1477 gtfl
A;Reference number: Z20854
A;Accession: T30552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Jaffe,
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                                                                                                                                                                 <u>р</u>ь
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                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:Z11873; A;Note: sequence extracted from N
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-1518 <GIF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glucosyltransferase (EC 2.4.1.-) I - Streptococcus salivarius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 12; Conserv
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Best Local
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NYAFVRAHDSEVQSII 624
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11; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #sequence_revision 22-Oct-1999 #text_change
                                                                                                                                                                                                                                                        68.4%;
70.6%;
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68.8%;
                                                                                                                                                                 620
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                                                                                                                                                                                                                                                                                                                                                                                                                      : NID:g47526; PIDN:CAA77900.1; PID:g47527
NCBI backbone (NCBIN:81050, NCBIP:81052)
                                                                                                                                                                                                                                     Score 65; DB
Pred. No. 0.01
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
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Pred. No.
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                                                                                                                                                                                                                                                        DB 2;
0.015;
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0.014;
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A;Accession: S22737
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1599 <JAC>
A;Cross-references: EMBL:Z11872; NID:g47530; PIDN:CAA77898.1; PID:g47531
A;Experimental source: ATCC 25975
A;Title: Eight genes and alternative RNA processing A;Reference number: S46326; MUID:94283388 A;Accession: S46329 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-575 <DOD>
                                                                                                                                                       intermediate filament protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 07-May 1995 #sequence_revision 21-Jul-1995 #te
C:Accession: S46329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glucosyltransferase - Streptococcus salivarius C;Species: Streptococcus salivarius C;Species: Streptococcus salivarius C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 C;Accession: T30858 R;Simpson, C.L.; Giffard, P.M.; Jacques, N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Giffard, P.M.; Simpson, C.L.; Milward, C.P.; Ja
J. Gen. Microbiol. 137, 2577-2593, 1991
A;Title: Molecular characterization of a cluster
A;Reference number: A44811; MUID:92148377
A;Accession: S28810
                                                                                                                      R; Dodemont, H.; Riemer, D.; EMBO J. 13, 2625-2638, 1994
                                                                                                                                                                                                                                         RESULT
S46329
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A;Molecule type: DNA
A;Residues: 1-1577 <SIM>
A:Cross-references: EMBL:L35928; NID:g662380; PID:g662381; PIDN:AAC41413.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Simpson, C.L., 509-621, 1995
Infect. Immun. 63, 609-621, 1995
A;Title: Streptococcus salivarius ATCC 25975 possesses
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A; Residues: 1-51 <GIF>
A; Cross-references: EMBL: Z11873
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Best Local S
Matches 11
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Best Local S
Matches 12
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eywords: glycosyltransferase; hexosyltransferase
456-1475/Domain: cpl repeat homology <CPR>
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                                                                                                                                                                                                                                                                                                                    661 NYIFVRAHDSEVQAVLA 677
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                                                                                                              2625-2638, 1994
                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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64.7%;
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70.68;
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                                                                                                                                      Ledger,
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Pred.
                                                                                                                                      N.; Weber,
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                                                                                                                                                                           21-Jul-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                              No.
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0.023;
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0.074;
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A;Title: DNA Sequence of both chromosomes of the
                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
G82455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
D86474
                                                                          A; Experimental C; Genetics:
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                                      A; Map position: 2
                                                          A; Gene: VCA0471
                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-51 <HEI>
                                                                                                                                                                                                               A; Reference number: A82035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position:
                                                                                                                                                                             A;Status:
                                                                                                                                                                                             A; Accession: G82455
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C;Accession: D86474

C;Accession: D86474

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dc ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E. C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Liuros, J.S.; Maiti, R.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Introns: 31/1; 125/3; 220/3; 252/3; 290/3; 348/3; 445/1; 471/3; C;Superfamily: intermediate filament protein Av71
                         Query Match
Best Local Similarity
Thehes 8; Conserve
                                                                                                                                                                                                                                         A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-327 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable RING zinc finger protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                     A; Cross-references: GB: AE005172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X70833; NID:g312743; PIDN:CAA50181.1; PID:g1848062
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4 YSFIRAHDSEVQDL
                                                  Conservative
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  17
                                                                       46.3%;
57.1%;
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66.7%;
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Pred. No. 8.3;
2; Mismatches
                                                                       Score 44; I
Pred. No. 9.
                                                  Mismatches
                                                                  DB
9.4;
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                                                  Indels
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hypothetical protein VCA0471 [imported] - Vibrio cholerae (strain N16961 serogroup O1 C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001 C;Accession: G82455 Clayton, R.A.; Bass, S.; Qin, Gwinn, M.L.; Do H.; Dragoi, I.; Dodson, R. I.; Sellers

MUID: 20406833

the cholera Bass,

pathogen Vibrio cholerae

A; Cross-references: source: GB:AE004379; ce: serogroup GB:AE003853; NID:g9657865; O1; strain N16961; biotype PIDN:AAF96375.1; GSPDB:GN El Tor

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Query Match 45.3%; Score 43; DB 2; Length 51;
Best Local Similarity 58.8%; Pred. No. 1.6;
Matches 10; Conservative 4; Mismatches 1; Indels 2; Gaps 1;
Qy 1 VPSYSFIRAHDSEVQDL 17
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Db 15 VPAYSAIR--NSEIRDL 29

Search completed: March 27, 2002, 14:01:16
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US-09-210-361-2  US-09-210-361-2  Sequence 2, Application US/09210361  Patent No. 6284479  GENERAL INFORMATION: APPLICANT: Nichols, Scott E. TITLE OF INVENTION: Substitutes for Modified Starches and TITLE OF INVENTION: Latexes in Paper Manufacture  FILE REFERENCE: 0357CR  CURRENT APPLICATION NUMBER: US/09/210,361  CURRENT FILING DATE: 1998-12-11  EARLIER APPLICATION NUMBER: 09/007,999  EARLIER APPLICATION NUMBER: 08/478,704  EARLIER FILING DATE: 1995-06-07  EARLIER FILING DATE: 1995-06-07  EARLIER FILING DATE: 1995-06-07  EARLIER FILING DATE: 1995-06-07  EARLIER FILING DATE: 1998-01-20  EARLIER FILING DATE: 1998-01-20  EARLIER FILING DATE: 1998-01-20  EARLIER FILING DATE: 1998-01-20  EARLIER FILING DATE: 1998-01-20	Query Match 100.0%; Score 112; DB 3; Length 1475; Best Local Similarity 100.0%; Pred. No. 9.3e-11; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gap Qy 1 TGARTTYCQLLYERANGVQVKG 22	RESULT 1  US-09-007-999-2  Sequence 2, Application US/09007999  Patent No. 6687559  GENERAL INFORMATION: SCOTT E.  TITLE OF INVENTION: Substitutes for Modified Starch and  TITLE OF INVENTION: Latexes in Paper Manufacture  FILE REFERENCE: 0356D Attexes in Paper Manufacture  CURRENT APPLICATION NUMBER: US/09/007,999  CURRENT FILING DATE: 1998-01-16  EARLIER APPLICATION NUMBER: 08/478,704  EARLIER FILING DATE: 1995-06-07  NUMBER OF SEO ID NOS: 2  SOFTWARE: FastSEQ for Windows Version 3.0  SEQ ID NO 2  LENGTH: 1475  TYPE: PRT  ORGANISM: Streptococcus mutans	ALIGNMENTS	28 46 41.1 648 2 US-08-467-852A-2 Sequence 2, 29 46 41.1 648 2 US-08-468-718-2 Sequence 2, 30 46 41.1 648 2 US-08-247-491A-2 Sequence 2, 31 46 41.1 695 1 US-08-127-499A-23 Sequence 2, 44.1 695 1 US-08-127-499A-23 Sequence 2, 34.1 695 1 US-08-08-127-499A-23 Sequence 4, 35.7 265 1 US-08-128-128-128-128-128-128-128-128-128-12
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EARLIER APPLICATION NUMBER: 09/008,172 EARLIER FILING DATE: 1998-01-16

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: FDO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/877,295
FILING DATE: 01-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINE FOR DENTAL CARIES NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                       Query Match
Best Local S
Matches 13
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EARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version :
SEQ ID NO 2
LENGTH: 1430
                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Nichols, Scott E.
TITLE OF INVENTION: Substitutes for modified Starch
TITLE OF INVENTION: Latexes in Paper Manufacture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09008172 Patent No. 6127602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 4 LENGTH: 1375
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Best Local (
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EARLIER FILING DATE: 1998-01-16
EARLIER APPLICATION NUMBER: 08/478,704
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 09/009,620
EARLIER FILING DATE: 1998-01-20
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CURRENT APPLICATION NUMBER: US/09/210,361
CURRENT FILING DATE: 1998-12-11
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EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 09/008,172
EARLIER FILING DATE: 1998-01-16
EARLIER APPLICATION NUMBER: 08/482,711
EARLIER FILING DATE: 1995-06-07
NUMBER OF SEO ID NOS: 6
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TITLE OF INVENTION: Latexes in Paper Manufacture
                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/008,172
CURRENT FILING DATE: 1998-01-16
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1332 TGSQTIAGKKLYFASDGKQVKG 1353
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                     1 TGARTINGQLLYFRANGVQVKG
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13; Conser
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15; Conserv
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59.1%;
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68.2%;
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Pred. No.
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Pred. No.
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                                                                       Mismatches
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                                                                                        DB 3;
                                                                                                           Length 1430;
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LENGTH: 1430
TYPE: PRT
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Best Local Similarity
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CURRENT FILING DATE: 1998-12-11
EARLIER APPLICATION NUMBER: 09/07,999
EARLIER FILING DATE: 1998-01-16
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EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 09/009,620
EARLIER FILING DATE: 1998-01-20
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EARLIER FILING DATE: 1995-06-07
ARLIER APPLICATION NUMBER: 09/008,172
ARLIER FILING DATE: 1998-01-16
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                                     CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/793,824
                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Jacques, TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Simpson, Christine Lynn
APPLICANT: Giffard, Philip Morrison
APPLICANT: Jacques, Nicholas Antho
                                                                                                                                                                                                                                                                                                                  STREET: Level 8, 168 Walker Street CITY: No. 5981838th Sydney
                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                        COUNTRY:
APPLICATION NUMBER: AU P
FILING DATE: 24-AUG-1994
                                                                                    FILING DATE:
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59.1%;
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Genetic Manipulation of Plants
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Pred. No. 0.
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US-08-793-824-2
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TELEX: 26547
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 08/422,711
FILING DATE: 14 APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
APPLICATION NUMBER: US 08/405,496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: PADHYE, NISHA V.
APPLICANT: ETRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND
TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
              APPLICATION NUMBER: 1
FILING DATE: 04-DEC-
PRIOR APPLICATION DATA:
                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
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LENGTH: 1577 amino acids
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                                                                      PRIOR APPLICATION DATA:
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                                                                                     APPLICATION NUMBER: US 0: FILING DATE: 02-DEC-1993
                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
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APPLICATION NUMBER:
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220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THALLEY, BRUCE S. PADHYE, NISHA V. FIRCA, JOSEPH R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNITED STATES OF AMERICA
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                                                                                                                                                                                            16-MAR-1995
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                                   04-DEC-1992
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                                                                                                       US 08/161,907
                                                                                                                                                         US 08/329,154
US 07/429,791
                                                   US 07/985,321
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US-08-405-496A-7; Sequence 7, Applic; Patent No. 5919665
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APPLICANT: WILLIA
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                  TELEFAX: (415) 397-83
INFORMATION FOR SEQ ID NO:
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SEQUENCE CHARACTERISTICS:
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TOPOLOGY: unk
MOLECULE TYPE:
                                                               REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
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MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 16-MAI
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STREET: 220 MONTGOMERY STREET,
CITY: SAN FRANCISCO
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                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
es 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08405496A
                                                                                                               INGOLIA, DIANE E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   811 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WILLIAMS, JAMES A.

IVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM 
VENTION: NEUROTOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (415) 397-8338
                                (415)
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                                                   (415) 705-8410
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                                                                                                                                                                                                                                                                                                                                                                   16-MAR-1995
                                                                                                                                                     JMBER: US 07/429,791
31-OCT-1989
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                              397-8338
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                                                                                    OPHD-01308
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Best Local Similarity
                    TELEFAX: (415) 397-83
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL
                                                                                                                           APPLICATION NUMBER: US 07/429,791 FILING DATE: 31-OCT-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 04-DEC-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                         FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT
TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08 FILING DATE: 02-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                REFERENCE/DOCKET NUMBER: OPHD-01763
                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                           INGOLIA, DIANE E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08915136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THALLEY, BRUCE S. PADHYE, NISHA V. FIRCA, JOSEPH R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNITED STATES OF AMERICA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLEN & CARROLL,
                                                                                                                                                                                                                                                                                                                                    NUMBER: US 08/405,496
16-MAR-1995
                                                                                                                                                                                       NUMBER: US 07/985,321
04-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
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                               397-8338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Release #1.0, Version #1.30
                                                                                                                                                                                                                                                          US 08/161,907
                                                                                                                                                                                                                                                                                                                                                                                                         08/480,604
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                                                                                             40,027
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Pred. No. 2.
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Length 812; Indels

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; TOPOLOGY: unknown.
; MOLECULE TYPE: protein
US-08-915-136-7
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US-08-480-604A-29
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Best Local Similarity
                                                                               FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPHE
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                      TELEFAX: (415) 397-83
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NOTATION
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/422,711 FILING DATE: 14-APR-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: THALLEY, BRUCE S.
APPLICANT: PANHYE, NISHA V.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT
TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 0 CLASSIFICATION:
                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/985,321 FILING DATE: 04-DEC-1992
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/329,154 FILING DATE: 25-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: SAN FRANCISCO
                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/480,604A
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                                                                    TELEPHONE:
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o. 5736139
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                                                    (415)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UNITED STATES OF AMERICA
                                                                    (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                       UMBER: US 07/429,791
31-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-1995
                                                                                                                                                                                                                                                                                02-DEC-1993
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                                                  397-8338
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                                    29:
                                                                                                       OPHD-01763
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Pred. No. 2
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US-08-915-136-29
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Patent No.
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                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
PRIOR APPLICATION UMBER: US
APPLICATION UMBER: US
FILING DATE: 16 MAR-15
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 25 -OCT - 15
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                  TELEFAX: (415) 397-83
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: un
TOPOLOGY: linear
MOLECULE TYPE: pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND
TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
              SEQUENCE CHARACTERISTICS:
                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                                                                                                                                                    FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/985,321 FILING DATE: 04-DEC-1992
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Local Similarity 52.2%;
hes 12; Conservative
                                                                                                     REGISTRATION NUMBER: 40,027 REFERENCE/DOCKET NUMBER: OP
                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 02-DEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: SAN FRANCISCO
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LENGTH:
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                                                                                                                                    INGOLIA, DIANE E
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02-DEC-1993
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                                                 397-8338
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Pred. No. 2.
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STRANDEDNESS: unknown TOPOLOGY: linear

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Best Local
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PRIOR APPLICATION DATA:
APPLICATION DATA: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/429,791
FILING DATE: 31-OCT-1989
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                                     TELEFAX: (415) 397-83: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        equence 6, Application US/08480604A atent No. 5736139
                                                                         REFERENCE/DOCKET NUMBER: OP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-0CT-1994
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APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-1995
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/422,711
FILING DATE: 14-APR-1995
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CURRENT APPLICATION DATA:
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TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND
TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                   REGISTRATION NUMBER:
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LENGTH:
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Similarity 52.2%;
                                                                                                                                                     INGOLIA, DIANE E.
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220 MONTGOMERY STREET, SUITE 2200
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                                                                                                                                   40,027
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Pred. No. 2
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                                                Matches
                                                             Query Match
Best Local
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Best Local Similarity 52.3
Matches 12; Conservative
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                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                 NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 25-OCT-:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 02-DEC--
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 0: FILING DATE: 25-OCT-1994
                                                           Local
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                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                       LENGTH:
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1 TGARTINGQLLYFRAN-GVQVKG 22
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                                                             Similarity
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VENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM
                                                                                                                                                                                       2710 amino acids
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                                                                                                                                                                                                                                       (415)
                                               Conservative
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                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                      NUMBER: US 07/985,321
04-DEC-1992
                                                                                                                                        protein
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                                                             44.2%; 52.2%;
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Pred. No. 1
                                                             Score 49.5;
Pred. No. 11;
                                               Mismatches
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                                                                          Length 2710;
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2460 TGLRTIDGKKYYFNTNTAVAVTG 2482

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; TELEFAX: (415) 397-8338;
; INFORMATION FOR SEQ ID NO: 6;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2710 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-915-136-6
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US-08-915-136-6
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PRIOR APPLICATION NUMBER: US 08/405,496
APPLICATION NUMBER: US 08/405,496
FILLING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
TITTING DATE: 25-OCT-1994
                                                                               Matches
                                                                                               Query Match
Best Local Similarity
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APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUC
APPLICANT: PADHYE, NISHA
                                                                                                                                                                                                                                                                                                                                    NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/429,791 FILING DATE: 31-OCT-1989 ATTORNEY/AGENT INFORMATION:
2460 TGLRTIDGKKYYFNTNTAVAVTG 2482
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APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
APPLICATION NUMBER: US 07/429,791
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,604
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
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APPLICANT: PANHYE, NISHA V.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                      1 TGARTINGQLLYFRAN-GVQVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSEE: MEDLEN & CARROLL, LLP
F: 220 MONTGOMERY STREET, SU
SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CALIFORNIA: UNITED STATES OF AMERICA
                                                                            Conservative
                                                                                               44.2%;
                                                                          Score 49.5; D
Pred. No. 11;
2; Mismatches
                                                                            2;
                                                                                                                                                                                                                                                                                                                                                                                OPHD-01763
                                     22
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                                                                                                                  DB 4;
                                                                            8;
                                                                                                                Length 2710;
                                                                            Indels
                                                                            1;
                                                                          Gaps
                                                                          1;
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Search completed: March 27, 2002, 13:59:28 Job time: 581 sec

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Page 8

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Result
No.
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein search, using sw model
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/cgn2_6/ptodata/2/paa/PCTUS_COMB_pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          March 27, 2002, 14:20:23; Search time 1139.61 Seconds (without alignments) 5.360 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-290-049A-3
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('gn2_6/ptodata/2/paa/US084_COMB.pep:*
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/paa/US07_COMB.pep:*
/cgn2_6/ptodata/2/paa/US08_COMB.pep:*
/cgn2_6/ptodata/2/paa/US081_COMB.pep:*
/cgn2_6/ptodata/2/paa/US083_COMB.pep:*
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        22
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    6 US-09-290-049-3
9 US-09-57-848-2
1 US-09-40-274-2
PCT-US93-04094-3
US-07-877-295-2
US-08-057-162-3
US-08-057-162A-3
6 US-09-288-965-3
1 US-09-740-274-4
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Sequence 2, Appli
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Sequence 2, Appli	sequence to	160, Ap	160,	1, Ap	4, App	6110,	872, 1	2538, A	6, Appl	6, Appl		e 6,	6, App	6, App	δ,	6, ₽	2, Appl	2, Appl	, m	e 29, App	equence 29, App	9, Appl	Sequence 7, Appli	7, Appl	7, Appl	e 7, App	7,	7, Appl	equence 7,	7, 1	3, Appl	1, App	2, Appl	e 6, App	, Appl

# ALIGNMENTS

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RESULT 1
US-09-290-049-3
US-09-290-049-3
US-09-290-049-3
US-09-290-049-3
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US-09-290-049
US-09-290-049-3
US-09-2
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TGARTINGQLLYFRANGVQVKG 22

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: Sequence 2, Application US/09557848

: GENERAL INFORMATION:
                                                                                                                                                                                                                             SOFTWARE: Fast
SEQ ID NO 2
LENGTH: 1475
                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SENERAL INFORMATION:
APPLICANT: Nichols, Scott E.
APPLICANT: Nichols, Scott E.
TITLE OF INVENTION: Glucan-containing Compositions and Paper
FILE REFERENCE: 0357CRD
CURRENT APPLICATION NUMBER: US/09/740,274
CURRENT FILING DATE: 2000-12-19
COURTENT FILING DATE: 2000-12-19
COURTENT FILING DATE: 201210,361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best
                                                                 Matches
                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1998-U1-20
PRIOR FILING DATE: 1998-U1-20
PRIOR APPLICATION NUMBER: 08/485,243
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 09/008,172
PRIOR APPLICATION NUMBER: 09/008,172
PRIOR PRIOR DATE: 1998-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/557,848 CURRENT FILING DATE: 2000-04-26 EARLIER APPLICATION NUMBER: 08/478,704 EARLIER FILING DATE: 1995-06-07 EARLIER APPLICATION NUMBER: 09/007,999 EARLIER FILING DATE: 1998-01-16 NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/210,361
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: 09/007,999
PRIOR FILING DATE: 1998-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Substitutes for Modified Starch and TITLE OF INVENTION: Latexes in Paper Manufacture FILE REFERENCE: 0356D2
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 08/478,704
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 09/09,620
PRIOR FILING DATE: 1998-01-20
PRIOR FILING DATE: 1998-01-20
                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 08/482,711 PRIOR FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Nichols,
                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 3.0 EQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1475
TYPE: PRT
ORGANISM: Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1300 TGARTINGQLLYFRANGVQVKG 1321
                                                          Local Similarity
nes 22; Conserv
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les 22; Conserv
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1 TGARTINGQLLYFRANGVQVKG 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09740274
                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                  100.0%; Score 112; 100.0%; Pred. No. :
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Pred. No. 2.1e-09;
0; Mismatches 0;
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                                                            2.1e-09;
hes 0;
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                                                                                                   Length 1475;
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Best Local Similarity
Matches 17; Conserva
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                                                                                                                                                                                                                                  Sequence 2, Application:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: FDC:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEPHAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1300 TGARTINGQLLYFRANGVQVKG 1321
                                                                                                                                        NUMBER OF SEQUENCES: 2
                                                                                                                                                                          APPLICANT: Taubman, Martin A.
APPLICANT: Smith, Daniel J.
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 1i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                       STREET: Two Mili
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 19930 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: AMINO /
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                COUNTRY: US
ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Granahan, Patricia. REGISTRATION NUMBER: 32,2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                            ADDRESSEE:
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                                                                               ΜA
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                                                                                                              Two Militia Drive
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                                                               USA
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                                                                                                                           Hamilton, Brook,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hamilton, Brook,
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77.38;
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CARIES
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                                                                                                                                                                                                                                                                                                                                                                                                            Score 87; I
Pred. No. 3.
                                                                                                                           Smith & Reynolds, P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith & Reynolds,
                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617) 861-95
INFORMATION FOR SEQ ID NO:
                                                                   TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ery Match
                                                                                                   FILING DATE: 01-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: FDC92-01A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                FILING DATE: 19930430 CLASSIFICATION: 424 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/057,162
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook,
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR TITLE OF INVENTION: CARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                              SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Taubman, Martin APPLICANT: Smith, Daniel J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Two Mil:
CITY: Lexington
STATE: Massachu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
SOFTWARE: Patentl
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Wagner, Richard W. REGISTRATION NUMBER: 34,480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: UPPLING DATE: 19920501
STRANDEDNESS:
                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/877,295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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|||:|| || || ||:|| || ||||
1 TGAQTIKGQKLYFKANGQQVKG
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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77.3%;
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Pred. No. 3.1e-07;
Nicmatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 22;
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; MOLECULE TYPE:
US-08-057-162A-3
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US-08-057-162A-3
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; MOLECULE TYPE:
US-08-057-162-3
RESULT 8
US-09-288-965-3
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                                                                                                                      Matches
                                                                                                                      Best Local Similarity Matches 17; Conserv
                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: FD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEPAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/877,295
FILING DATE: 01-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Wagner, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                             SEQUENCE CVARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Taubman, Martin A. APPLICANT: Smith, Daniel J.
                                                                                                                                                                                                                                                                                                                                                                                     NAME: Wagner, Richard
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 30-APR CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Two Mili
                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                        1 TGAQTIKGQKLYFKANGQQVKG
                                                                            1 TGARTINGQLLYFRANGVQVKG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TGARTINGQLLYFRANGVQVKG 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                        Conservative
                                                                                                                                                                                                                                ss: single
linear
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30~APR-1993
                                                                                                                                                                                                                  peptide
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77.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Daniel J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYNTHETIC PEPTIDE VACCINE FOR DENTAL
                                                                                                                                      77.78;
77.38;
                                                                                                                                                                                                                                                                                                                                                                                     34,480
                                                                                                                                      Score 87; DB 4;
Pred. No. 3.1e-07;
                                                                                                                                                                                                                                                                                                                                                                          FDC92-01A
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Pred. No. 3.1e-07;
                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                   Length 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 22;
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                                                                                                                        Gaps
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Sequence 3, Application US/09288965 GENERAL INFORMATION: APPLICANT: Lees, Andrew

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PRIOR FILING DATE: 09/007, yyy
PRIOR APPLICATION NUMBER: 09/007, yyy
PRIOR FILING DATE: 1998-01-16
PRIOR PRIOR TILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 09/009,620
US-09-649-885-2; Sequence 2, Applicat; GENERAL INFORMATION:
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                                                                         RESULT
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                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 15; Conserv
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LENGTH: 1375
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TITLE OF INVENTION: CONJUGATE VACCINES FOR THE PREVENTION OF DENTAL CARIES FILE REFERENCE: 04995-0046-00000

CURRENT APPLICATION NUMBER: US/09/288,965

CURRENT FILING DATE: 1999-04-09

EARLIER APPLICATION UMBER: 60/081,315

EARLIER FILING DATE: 1998-04-10

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PATENTION OF SEQ ID NOS: 19

ENGIT: 22

TYPE: PRT
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CURRENT APPLICATION NUMBER: US/09/740,274
CURRENT FILING DATE: 2000-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Nichols, Scott E.
TITLE OF INVENTION: Glucan-containing Compositions and Paper
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 08/0 PRIOR FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 1998-12-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: may be S. mutans, 09-288-965-3
                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Taubman, Martin A.
                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                1 TGARTINGQLLYFRANGVQVKG 22
|| | || || || || || || 1
1264 TGTVTFNGQRLYFKPNGVQAKG 1285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity les 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1998-U1-20
RAPPLICATION NUMBER: 08/485,243
PTITHG DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 09/008,172 FILING DATE: 1998-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGAQTIKGQKLYFKANGQQVKG 22
                                  Application US/09649885
                                                                                                                                                                                                                                                                                                                                                                                                            FastSEQ
                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                   69.6%;
68.2%;
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                                                                                                                                                                                                                               Score 78;
Pred. No.
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Pred.
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                                                                                                                                                                                                         Mismatches
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3.1e-07;
hes 3;
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FILE REPRENCE: 0358D2
CURRENT APPLICATION NUMBER: US/09/649,885.
CURRENT FILING DATE: 2000-08-28
PRIOR APPLICATION NUMBER: US 09/008,172
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 08/482,711
PRIOR FILING DATE: 1995-06-07
                                                                                                                                                      ; ORGANISM: streptococcus mutans US-09-740-274-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Streptococcus mutans US-09-649-885-2
                                                                                                                                                                                                                   NUMBER OF SEQ ID SOFTWARE: FastSE SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/09740274 GENERAL INFORMATION:
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SEQ ID NO 2
                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING LANGE 1997.

PRIOR APPLICATION NUMBER: 09/2.

PRIOR APPLICATION NUMBER: 09/0

PRIOR APPLICATION NUMBER: 09/0

PRIOR APPLICATION NUMBER: 09/0

OR //
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/740,274
CURRENT FILING DATE: 2000-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Nichols, Scott E.
TITLE OF INVENTION: Glucan-c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Nichols, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/0
PRIOR FILING DATE: 1998-01-16
                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1998-PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1995-
                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 09/U
                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 08/478,704 PRIOR FILING DATE: 1995-06-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE:
                                                                                                                                                                                                                                                                          PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                      LENGTH: 1430
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||::|| |: ||| ::| ||||
1332 TGSQTIAGKKLYFASDGKQVKG
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1332 TGSQTIAGKKLYFASDGKQVKG 1353
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                                                                                 Local Similarity
                 1 TGARTINGQLLYFRANGVQVKG 22
                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/0
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                                                                 Conservative
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                                                                                 59.8%;
59.1%;
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59.1%;
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1353
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                                                                               Score 67; I
Pred. No. 0.
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Pred. No.
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RESULT 12
US-09-499-203-2
: Sequence 2, Application US/09499203
; GENERAL INFORMATION:

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Query Match
Best Local Similarity
Thes 12; Conserve
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US-09-446-269-3
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                                            Sequence 3, Application US/09446269
GENERAL INFORMATION:
APPLICANT: WAED, STEPHEN J.
APPLICANT: WREN, BRENDAN W.
APPLICANT: DOUGAN, GORDON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/499,203
CURRENT FILING DATE: 2000-02-08
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 2057
                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 1
LENGTH: 320
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APPLICANT:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/446,269
CURRENT FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/GB98/01805
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: GB 9713146.0
PRIOR FILING DATE: 1997-06-20
PRIOR FILING DATE: 1998-01-07
PRIOR FILING DATE: 1998-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
TITLE OF INVENTION: IMMUNUSARITITE OF INVENTION: DIFFICILE
TITLE OF INVENTION: DIFFICILE
TITLE OF INVENTION: INVENTION: IIS
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APPLICANT: WELSH, Thomas
APPLICANT: QUANZ, Martin
APPLICANT: KNUTH, Karola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Nucleic Acid Molecules Encoding Alternansucrase FILE REFERENCE: 147-196P
TITLE OF INVENTION: IMMUNOGENIC FRAGMENTS OF TOXIN A TITLE OF INVENTION: DIFFICILE
                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: SOFTWARE: PatentIn V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Clostridium difficile 9-446-269-1
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                                                                                                                                                                                                GARTINGQLLYFRANGVQVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Ver. 2.0
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DOUCE, GILL
                               DOUGAN, GORDON DOUCE, GILL
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57.1%;
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Pred. No. 16
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0.3;
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               OF.
               CLOSTRIDIUM
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; LENGTH: 457
; TYPE: PRT
; ORGANISM: Clostridium difficile
US-09-446-269-3
Query Match
Best Local Similarity
Watches 12; Conserva
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GENERAL INFORMATION:
APPLICANT: Williams, James A.
APPLICANT: Thalley, Bruce S.
TITLE OF INVENTION: Multivalent Vaccine For Clostridium
TITLE OF INVENTION: Botulinum Neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity 52.2%;
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PRIOR FILING DATE: 1997-06-20
PRIOR APPLICATION NUMBER: GB 9800321.3
PRIOR FILING DATE: 1998-01-07
NUMBER OF SEQ ID NOS: 7
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CURRENT FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/GB98/01805
PRIOR FILING DATE: 1998-06-19
                                                                                                                                                                                                                           TELEPHONE: (415) 705-
TELEFAX: (415) 397-83
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE:
                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 811 amino acids
                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: OP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 TGLRTIDGKKYYFNTNTAVAVTG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                     TYPE: amino a
                                                                                                                                                                                                                                                                                                                  NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING TOTAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Medlen & Caliform
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                      CLASSIF LCATION:
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(415) 39
                Conservative
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52.2%;
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                               Score 49.5;
Pred. No. 4
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Pred. No. 2
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                Mismatches
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                Indels
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Search completed: March 27, 2002, 14:20:24 Job time: 1571 sec

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
          40.5
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1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*

8: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
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        Match
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Gapop 10.0 , Gapext 0
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112
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    US-09-562-328-37
US-09-290-049A-3
US-09-562-328-7
US-09-562-328-4
US-09-562-328-7
US-09-562-328-7
US-10-011-366-6
US-09-708-427-10858
US-09-708-427-3068
US-09-848-909-26
US-09-848-909-32
US-09-848-999-32
US-09-848-7990-32
US-09-848-7990-32
US-09-675-784A-7990-32
US-09-675-784A-7990-32
US-09-60-44-933-106
US-10-015-127-9902
US-09-604-6933-106
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Sequence 37, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 6, Appli Sequence 10858, A Sequence 10858, A Sequence 970, App Sequence 30687, A Sequence 30686, A Sequence 30686, A Sequence 26, Appli Sequence 26, Appli Sequence 31, Appli Sequence 50, Appli Sequence 4915, Appli Sequence 4915, Appli Sequence 4915, Appli Sequence 4915, Appli Sequence 3002, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
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RESULT 2 US-09-290-049A-3 US-09-290-049A-3 Sequence 3, Application US/09290049A Sequence 3, Application US/09290049A GENERAL INFORMATION: APPLICANT: Smith, Daniel J. APPLICANT: TAUDMAN, Martin A. TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL TITLE OF INVENTION: CARLES FILE REFERENCE: 1564.1008-002 CURRENT APPLICATION NUMBER: US/09/290,049A CURRENT FILING DATE: 1999-04-12 PRIOR APPLICATION NUMBER: 60/081,550 PRIOR APPLICATION NUMBER: 60/081,550 PRIOR FILING DATE: 1999-04-04 PRIOR FILING DATE: 1999-01-08 NUMBER OF SEQ ID NOS: 19 SOFTWARE: FastSEQ for Windows Version 4.0	Query Match Query Match Query Match Query Match Best Local Similarity 100.0%; Pred. No. 2.8e-12; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps Qy 1 TGARTINGOLLYFRANGYQVKG 22 Qy 1 TGARTINGQLLYFRANGYQVKG 22	RESULT 1 US-09-562-328-37 US-09-562-328-37 INSON-562-328-37 INSON-562-328-37 US-09-562-328-37 US-09-562-328-37 US-09-562-328-37 US-09-562-328-37 US-09-562-328-37	ALIGNMENTS	26 40 35.7 19 6 US-09-562-328-39 Sequence 39, A 35.7 169 6 US-09-605-703B-1180 Sequence 1180, 28 40 35.7 231 6 US-09-605-703B-1180 Sequence 17, A 29 40 35.7 266 US-09-708-427-17269 Sequence 1726 30 40 35.7 363 6 US-09-708-427-17269 Sequence 1726 31 40 35.7 369 6 US-09-605-703B-1178 Sequence 1726 31 40 35.7 400 6 US-09-605-703B-1178 Sequence 1726 31 40 35.7 590 6 US-09-708-427-9653 Sequence 1726 31 40 35.7 590 6 US-09-708-427-9653 Sequence 1726 31 40 35.7 590 6 US-09-708-427-9652 Sequence 2726 31 30 40 35.7 669 6 US-09-708-427-9651 Sequence 2726 31 30 39.8 31 30 4 7 US-10-015-127-11175 Sequence 2726 31 30 39.8 31 39 34.8 31 37 6 US-09-708-427-964 Sequence 2726 31 30 39 34.8 31 39 39 34.8 31 39 39 39 39 39 39 39 39 39 39 39 39 39
	iaps 0	CARIES		' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' '

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SEQ ID NO 3
LENGTH: 22
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:

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                                                                             ; TYPE: PRT; ORGANISM: Streptococcus sp. US-09-562-328-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: GLB peptide US-09-290-049A-3
                                                                                                                                                                                                                                                                                                                                                                                                         US-09-562-328-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Streptococcus sp. US-09-562-328-7
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Best Local Similarity
Matches 17; Conserv
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APPLICANT: LEES, ANDREW
APPLICANT: TAUBMAN, MARTIN A.
APPLICANT: SMITH, DANIEL J.
APPLICANT: SMITH, DANIEL J.
TITLE OF INVENTION: CONJUGATE VACCINES FOR THE PREVENTION OF DENTAL CARIES
FILE REFERENCE: 04995.0046-01
FILE REFERENCE: 04995.0046-01
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     Sequence 43, Application US/09562328 GENERAL INFORMATION:
                                                                                                                                 SEQ ID NO 43
LENGTH: 26
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LENGTH: 22
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Best Local
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                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/562,328
CURRENT FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 09/288,965
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                             APPLICANT: LEES, ANDREW APPLICANT: TAUBMAN, MARTIN A. APPLICANT: TAUBMAN, MARTIN A. APPLICANT: SMITH, DANIEL J. TITLE OF INVENTION: CONJUGATE VACCINES FOR THE PREVENTION OF DENTAL CARIES FILE REFERENCE: 04995.0046-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/56:
CURRENT FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 09/288,965
                                                                                                                                                                     SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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les 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TGAQTIKGQKLYFKANGQQVKG
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     77.7%;
77.3%;
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Pred. No.
2; Mismatc
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     Score
Pred.
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     87; DB 6;
No. 5.3e-08;
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ches 3;
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US-10-011-366-6

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US-10-011-366-7; Sequence 7, Application US/10011366; GENERAL IMFORMATION:
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Best Local S
Matches 12
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                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 7:
587 TGLRTIDGKKYYFNTNTAVAVTG 609
                                   1 TGARTINGQLLYFRAN-GVQVKG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TGARTINGQLLYFRANGVQVKG 22
                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 811 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                         MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                           TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Medlen & Carroll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: IDENTIFICATION OF NEUTRALIZING EPITOPES
OF TOXIN A AND TOXIN B FOR THE TREATMENT OF C. DIFFICILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Williams, James A.
Kink, John A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGAQTIKGQKLYFKANGQQVKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/957,310
FILING DATE: 23-0CT-1997
APPLICATION NUMBER: US 08/329,154
FILING DATE: 24-0CT-1994
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-0EC-1993
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-0EC-1992
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-0CT-1989
                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027 REFERENCE/DOCKET NUMBER: OP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/011,366 FILING DATE: 16-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                            Conservative
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                                                                                            44.2%;
52.2%;
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                                                                                            Score 49.5;
Pred. No. 6.
                                                                            Mismatches
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                                                                                                              DB 7; Length 811;
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                                                                                                                                                               US-09-708-427-10858 Sequence 10858, Application US/09708427 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                           Matches
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
                                                                               APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THERENY
FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                                                                                                                                                                                                uery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                            2460 TGLRTIDGKKYYFNTNTAVAVTG 2482
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APPLICATION NUMBER: US/10/011,366
FILING DATE: 16-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPHD-01121
TELECOMMUNICATION INFORMATION:
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Kink, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                              TGARTINGQLLYFRAN-GVQVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/957,310 FILING DATE: 23-CCT-1997 APPLICATION NUMBER: US 08/329,154 FILING DATE: 24-CCT-1994 APPLICATION NUMBER: US 08/161,907 FILING DATE: 02-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: .IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/429,791 FILING DATE: 31-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 220 Montgomery Street, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 2710 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/985,321 FILING DATE: 04-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Medlen & Carroll
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISEASE
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Pred. No. 25;
2; Mismatches
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; NAME/KEY: misc_feature
LOCATION: 1.563
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: 1.563
; OTHER INFORMATION: Ceres Seq. ID 1822113
US-09-708-427-10858
                                                                                                                                                                                                                                            RESULT
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Best Local Similarity
"hes 10; Conserva
                                                                                                                                                                                                                          US-10-091-504-970
SOFTWARE: Pat
SEQ ID NO 970
LENGTH: 115
TYPE: PRT
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                        Sequence 970, Application US/10091504 GENERAL INFORMATION:
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SEQ ID NO 10857
LENGTH: 630
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                                                                               APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC007C1
CURRENT APPLICATION NUMBER: US/10/091,504
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
                                                  Prior Application removed - SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: N. ALEXANDROV et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1..630
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Ceres Seq. ID 1822112
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Pred. No. 26;
3; Mismatches
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Pred. No.
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RESULT 10
US-09-621-976-4566
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: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-091-504-970
                                                                                        ; ORGANISM: Homo sapiens US-09-621-976-4566
Ouery Match
Best Local Similarity
Matches, 7; Conserv
                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Dumas wilne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human
FILE REFERENCE: GENSET.054PR2
                                                                                                                                         NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 4566
LENGTH: 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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CURRENT FILING DATE: 2000-07-21
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
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OTHER INFORMATION: Xaa equals
NAME/KEY: misc_feature
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OTHER INFORMATION: Xaa
NAME/KEY: misc_feature
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OTHER INFORMATION: xaa equals
NAME/KEY: misc_feature
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OTHER INFORMATION: Xaa
NAME/KEY: misc_feature
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OTHER INFORMATION: Xaa
NAME/KEY: misc_feature
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NAME/KDY: misc_feature
LOCATION: (30)
OTHER INFORMATION: Xaa equals
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OTHER INFORMATION: Xaa
NAME/KEY: misc_feature
LOCATION: (8)
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milarity 70.0%;
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   ; Score 44; DB; Pred. No. 6.8; 3; Mismatches
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Pred. No. 5.1;
3; Mismatches
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APPLICANT: N. ALEXANDROV et al.
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FR.
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243p
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIN version 3.1
SEQ ID NO 30687
LENGTH: 1684
TYPE: PRT
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US-09-708-427-30687
; Sequence 30687, Application US/09708427
; GENERAL INFORMATION:
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Best Local Similarity
% 8; Conserva
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 30688
LENGTH: 1675
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                                              Query Match
Best Local Similarity
Matches 8; Conser
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OTHER INFORMATION: Xaa
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OTHER INFORMATION: Xaa
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1 TGARTINGQLLYFRA 15
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Pred. No.
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Pred. No. 1.2e+02;
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890 TLARTVRGMMYYYRA 904

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CURRENT APPLICATION NUMBER: US/09/605,703B
LURRENT FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/142,764
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: 60/152,318
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 2934
SEQ ID NO 1602
LENGTH: 152
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                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-605-703B-1602
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US-09-708-427-30686
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US-09-605-703B-1602
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SEQUENCE 30686, Application US/09708427

SEQUENCE 30686, Application US/09708427

APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: THEREBY

FILE REFERENCE: 2750-11439

CURRENT APPLICATION UNMBER: US/09/708,427

CURRENT FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SOFTWARE: PatentIn version 3.1

SEQ ID NO 30666

LENGTH: 1780
                                                                        Query Match 38.8
Best Local Similarity 54.5
Matches 12; Conservative
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Best Local Similarity
Matches 8; Conservat
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APPLICANT: Kroger, Burkhard
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORVIEDACTERIUM GLUTAMICUM GENES ENCODING NOVEL
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: BGI-129CP
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OTHER INFORMATION: Xaa is any amino acid
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ORGANISM: Arabidopsis thaliana
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TGA-TISASANVLRAAGVQVRG 145
                                    TGARTINGQLLYFRANGVQVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schroder, Hartwig
Zelder, Oskar
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                                                                                          38.8%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.3%;
53.3%;
                                                                        Score 43.5; DE Pred. No. 8.5; 2; Mismatches
                                    22
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Pred. No. 1.3e+02;
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                                                                                                              6;
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                                                                                                            Length 152;
                                                                          Indels
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Sequence 26, Application US/09848909
GENERAL INFORMATION:
APPLICANT: Collier, R. John
APPLICANT: Sellman, Brett R.
TITLE OF INVENTION: Compounds and Methods for the Treatment TITLE OF INVENTION: Compounds and Methods for the Treatment FILE REFERENCE: 00742/060002
CURRENT APPLICATION NUMBER: US/09/848,909
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/201,800
PRIOR APPLICATION NUMBER: US 60/201,800
PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                                ; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 706
; TYPE: PRT
; ORGANISM: Clostridium perfringens
US-09-848-909-26
Search completed: March 27, Job time: 1693 sec
                                                                                                         В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-848-909-26
                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 9; Conserva
                                                                                                       388 TKNGELLYF -- NGIPI 401
                                                                                                                                                 5 TINGQLLYFRANGVQV 20
                                                                                                                                                                                           Conservative
                                                                                                                                                                                                             38.4%; 56.2%;
                      2002, 14:22:46
                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                     6;
                                                                                                                                                                                                                                     Length 706
                                                                                                                                                                                             Indels
                                                                                                                                                                                           2;
                                                                                                                                                                                           Gaps
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Title: Perfect score: Run on: OM protein - protein search, using sw model March 27, 2002, 14:01:16; Search time 102.51 Seconds (without alignments) 16.348 Million cell updates/sec US-09-290-049A-3 GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

Scoring table: TGARTINGQLLYFRANGVQVKG 22

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters:

219241

mum DB seq length: 0 mum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_68:\*

1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	0	տ	4	ω	2	1	No.	7
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40.2	40.2	41.1	41.1	41.1	41.1	41.1	41.1	42.0	42.0		44.2	44.2	44.6	48.2	œ	58.9	59.8	60.7	60.7	64.3	65.2	67.0	67.0	69.6	71.4	73.2	77.7	100.0	Match	2
648	630	2364	1301	619	301	245	231	788	696	126	2710	529	831	221	329	1577	1431	1449	563	1508	1449	1365	1290	1375	1518	1599	1592	1475	Length	
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S10869	T05433	I40884	S18118	A41971	S13165	F64465	F70471	JS0747	A29635	S40016	A37052	T10388	T00323	T37244	A55221	T30858	A45866	T30552	A37184	T31098	T30857	A41483	JC5473	JT0345	A44811	S22737	A38175	в33135	ID	
enterotoxin A - Cl	hypothetical prote	cytotoxin L - Clos	alpha-amylase - Al	surface protein ps	asialoglycoprotein	hypothetical prote	conserved hypothet	regulatory protein	transcription fact	doc protein - phag	toxin A - Clostrid	hypothetical prote	chitinase (EC 3.2.	GATA transcription	detranase inhibito	glucosyltransferas	dextransucrase (EC	glucosyltransferas	glucan-binding pro	probable dextransu	glucosyltransferas	O .		dextransucrase (EC	glucosyltransferas	glucosyltransferas		gtfB protein precu	Description	

RESULT 2
A38175
Glucosyltransferase precursor - Streptococcus sobrinus
C;Species: Streptococcus sobrinus
C;Species: Streptococcus sobrinus
C;Species: Streptococcus sobrinus
C;Dete: 28-Aug-1992 #sequence\_revision 28-Aug-1992 #text\_change 15-Oct-1999
C;Accession: A38175
R;Abo, H.; Mtsumura, T.; Kodama, T.; Ohta, H.; Fukui, K.; Kato, K.; Kagawa, H.
J. Bacteriol. 173, 989-996, 1991
A;Title: Peptide sequences for sucrose splitting and glucan binding within Streptococ
A;Reference number: A38175; MUID:91123227
A;Accession: A38175

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	J.C
43	43	43	43	43	43	44	44	44	44	44	44	44	44	44	44
38.4	38.4	38.4	38.4	38.4	38.4	39.3	39.3	39.3	39.3	39.3	39.3	39.3	39.3	39.3	39.3
509	467	329	305	299	110	2178	1780	1679	1396	829	591	566	522	522	229
Ν	<b>-</b>	N	N	N	N	N	N	N	N	N	N	2	2	Ν	^
A49094	S45493	H75117	B75474	T15928	B69403	S55805	A85045	T30271	S36851	T29372	C84220	S74633	H75135	D71074	F/IU14
						•									

### ALIGNMENTS

Qy 1 TGARTINGQLLYFRANGVQVKG 22 	Query Match 100.0%; Score 112; DB 2; Length 1475; Best Local Similarity 100.0%; Pred. No. 4.9e-10; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	repeat repeat repeat	C;Superfamily: cpl repeat homology F;1096-1115/Domain: cpl repeat homology <cpl> F;1224-1243/Domain: cpl repeat homology <cp2></cp2></cpl>	A; Forecute type: NWA A; Forecomes 1 -171,173-641,'N', 643-1475 <sh2> A; Experimental source: strain GS-5</sh2>	A;Accession: A33129 A;Status: preliminary; not compared with conceptual translation	submitted to the Protein Sequence Database, September 1990  A; Reference number: A33128	A; MOLECULE type: DNA A; Residues: 1-1475 <shi> A; Cross-references: GS:M17361; NID:g153639; PIDN:AAA88588.1; PID:g153640</shi>	A; Status: preliminary	J. Bacteriol. 169, 4263-4270, 1987 A;Title: Sequence analysis of the gtfB gene from Streptococcus mutans. A;Reference number: A33135; MUID:87308013	c; Accession: B33135; A33128 R; Shiroza, T.; Ueda, S.; Kuramitsu, H.K.	gtfB protein precursor - Streptococcus mutans C:Species: Streptococcus mutans	RESULT 1 B33135
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A; Molecule type: DNA
A; Residues: 1-1592 ABD>
A; Residues: 1-1592 ABD>
A; Cross-references: GB:D902
C; Superfamily: cpl repeat h
F; 1093-1112/Domain: cpl rep
F; 1287-1306/Domain: cpl rep
F; 1287-1310/Domain: cpl rep
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A; Residues: 1-1599 < 2AC>
A; Cross-references: EMBL:Z11872; NID:g47530; PIDN:CAA77898.1; PID:g47531
A; Experimental source: ATCC 25975
A; Experimental source: C.L.; Milward, C.P.; Jacques, N.A.
J. Gen. Microbiol. 137, 2577-2593, 1991
A; Title: Molecular characterization of a cluster of at least two glucosy A; Reference number: A44811; MUID:92148377
A; Accession: S28810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Jacques, N.
submitted to the EMBL Data submitted to the EMBL Data submitted to the EMBL Data
                                                                                 glucosyltransferase (EC 2.4.1.-) I - Streptococcus salivarius C;Species: Streptococcus salivarius C;Species: Streptococcus salivarius C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change C;Accession: A44811; S22726; S28809 R;Giffard, P.M.; Simpson, C.L.; Milward, C.P.; Jacques, N.A.
                                                                                                                                                                                                                                                   Вb
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C;Keywords: glycosyltransferase; hexosy:
F;1456-1475/Domain: cpl repeat homology
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C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992
C;Accession: S22737; S28810; B44811; S22727
                  A; Reference number: A44811;
A; Accession: A44811
                                                   J. Gen. Microbiol. 137, 2577-2593, 1991
A; Title: Molecular characterization of a cluster
                                                                                                                                                                               A44811
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A; Residues: 1-51 <GIF>
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F;1513-1532/Domain:
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A; Molecule type:
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Best Local
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02 TGAQVINGQHLYFDANGRQVKG 14:
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No.
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A;Residues: 1-1518 <GIF>
A;Cross references: EMBL:/
A;Note: sequence extracted
C;Genetics:
A;Gene: gtfJ
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C;Keywords: glycosyltransferase; hexosyltransferase
F;1307-1326/Domain: cpl repeat homology <CP4>
                                                                                                                                                                                                                                                                                              A; Description: catalyzes the synthesis of both water-soluble and C; Superfamily: cpl repeat homology C; Keywords: duplication; glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: GS-5
R; Shiroza, T; Ueda, S; Kuramitsu, H.K.
J. Bacteriol. 169, 4263-4770, 1987
A; Title: Sequence analysis of the gtfB gene
A; Reference number: A33135; MUID:87308013
A; Accession: C33135
A; Status: preliminary
                                                                                    οy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: JT0345; C
R; Ueda, S.; Shiroza, T
Gene 69, 101-109, 1988
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                                                   дb
                                                                                                                                                                                                        F;1126-1145/Domain: cpl repeat homology <CPl>
F;1253-1272/Domain: cpl repeat homology <CP2>
F;1318-1337/Domain: cpl repeat homology <CP3>
                                                                                                                                                                                                                                                             F;35-1375/Product: glucosytransferase #status predicted <NAT>
                                                                                                                                                                                                                                                                                                                                                   C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Streptococcus mutans
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 24-Sep-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-349 <SHI>
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A; Residues: 1-1375 <UED>
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Best Local Similarity
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                                                                                                                         Conservative
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sucrose 6-glucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL:Z11873; NID:g47526; PIDN:CAA77900.1; PID:g47527 tracted from NCBI backbone (NCBIN:81050, NCBIP:81052)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kuramitsu,
                                                                                                                                     69.6%;
68.2%;
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72.78;
                                                   1285
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Pred.
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Pred.
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                                                                                                                       Mismatches
                                                                                                                                       78;
No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from
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                                                                                                                                       DB 2;
0.00018,
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9.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1518;
                                                                                                                                                      Length 1375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                      water-insoluble
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gluc

dextransucrase (EC 2.4.1.5) - Leuconostoc mesenteroides
C;Species: Leuconostoc mesenteroides
C;Species: Leuconostoc mesenteroides
C;Date: 07-Jul-1997 #sequence\_revision 29-Aug-1997 #text\_change 29-Aug-1997
C;Accession: JC5473
R;Monchois, V; Willemot, R.M.; Remaud-Simeon, M.; Croux, C.; Monsan, P.

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A;Title: Cloning and sequencing of a gene coding A;Reference number: JC5473; MUID:9713686 A;Accession: JC5473 A;Status: nucleic acid sequence not shown; transl A;Status: nucleic acid sequence not shown;
                                                                                                                                                                                                                          glucosyltransferase - Streptococcus salivarius C;Species: Streptococcus salivarius C;Date: 22-oct-1999 #sequence_revision 22-oct-C;Accession: T30857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
"~+~hes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Keywords: glycosyltransferase; hexosyltransferase F;78-870/Domain: catalytic #status predicted <CAT> F;922-1290/Domain: glucan-binding #status predicted
                                                                                                A; Molecule type: DNA
A; Residues: 1-1449 <
                                                                                                                                              A; Reference number: Z20909; A; Accession: T30857
                                                                                                                                                             A; Title: Streptococcus salivarius ATCC 25975 possesses A; Reference number: Z20909; MUID:95122197
                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: cpl repeat homology
C;Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-1365 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Infect. Immun. 58, 2452-2458, 1990
A;Title: Analysis of the Streptococcus downei
A;Reference number: A41483; MUID:90316665
A;Accession: A41483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glucosyltransferase (EC 2.4.1.-) gtfS precursor - C;Species: Streptococonia sobrisor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:U38181
C;Comment: This enzyme catalyzes
                                                 A; Gene:
                                                                               A; Cross-references:
                                                                                                                               A; Status: preliminary; translated
                                                                                                                                                                                               Infect. Immun. 63, 609-621,
                                                                                                                                                                                                           R; Simpson, C.L.;
                                                                                                                                                                                                                                                                                               T30857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GB:M30943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Gilmore, K.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Species: Streptococcus sobrinus;Date: 30-Jun-1992 #sequence_rev;Accession: A41483
Query Match
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                            Giffard, P.M.; Jacques, N.A.
3, 609-621, 1995
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                                                                             <SIM>
: EMBL:L35495;
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68.2%;
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63.6%;
 65.2%;
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Pred. No.
5; Mismatc
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                                                                               NID:g662378;
                                                                                                                               from
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Pred. No. 0.00053;
Score
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                                                                                                                               GB/EMBL/DDBJ
                                                                                                                                                                                                                                             22-oct-1999
73;
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DB
                                                                             PID:g662379;
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2;
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Length 1449;
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                                                                             PIDN: AAC41412.1
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RESULT
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R:Banas, J.A.; Russell, R.R.B
Infect. Immun. 58, 667-673, 19
A:Title: Sequence analysis of
A:Reference numbor: A37184; MC
A:Accession: A37787
                                                                                                                              C;Superfamily: cpl repeat homology CPl> F;169-188/Domain: cpl repeat homology CPP> F;264-283/Domain: cpl repeat homology CP2> F;349-368/Domain: cpl repeat homology CP3> F;504-523/Domain: cpl repeat homology CP4> F;525-548/Domain: cpl repeat homology CP4>
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
A37184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R:Monchois, V.; Remaud-Simeon, M.; Monsan, FEMS Microbiol. Lett. 159, 307-315, 1998 A;Title: Cloning and sequencing of a gene c A;Reference number: Z20981; MUID:98164374 A;Accession: T31098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Keywords:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Function:
A; Description:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-1508 < MON>
A; Cross-references: EMBL
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 B
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C; Date: 31-Jan-1992 #sequence_revision 31-Jan-1992
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C; Date: 22-Oct-1999
                                                                                                                                                                                                                     A; Cross-references: GB:M30945; NID:g153637;
                                                                                                                                                                                                                                   A; Residues:
                                                                                                                                                                                                                                                   A; Molecule type: UNA
                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                        C; Accession: A37184
                                                                                                                                                                                                                                                                                                                                                                                                   glucan-binding protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable dextransucrase (EC 2.4.1.5)
C; Species: Leuconostoc mesenteroides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 64.3
Best Local Similarity 68.3
Matches 15; Conservative
                                                                        Query Match
Best Local
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                                                          Matches
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                  GARTINGQLLYFRANGVQVKG
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 GWRTIGGKKYYFDTNGVQVKG
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glycosyltransferase;
                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source: strain
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                                                          Conservative
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ce: strain NRRL
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                                                                                                                                                                                                                                                                                                                                       R.R.B.;
                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.3%;
68.2%;
                                                                         66
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                                                                                                                                                                                                                                                                                              of the gene for MUID:90170123
                                                                                                                                                                                                                                                                                                                            1990
                                                                        . 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          composed only of alpha(1-6) glucosidic hexosyltransferase
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296
                             22
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                                                       Score 68; DB Pred. No. 0.00 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22
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Pred.
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2; Mismatches
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B-1299
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No.
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0.002;
                                                                                                                                                                                                                       PIDN:AAA26894.1; PID:g153638
                                                                        DB 2;
                                                                                                                                                                                                                                                                                                           glucan-binding
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                                                          6;
                                                                                    Length 563;
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RESULT
T30858
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J. Gen. Microbiol. 136, 2099-2105, 1990
A;Title: Nucleotide sequence of the Streptococcus mutans gtfD gene encoding the glucosyl
A;Reference number: A45866; MUID:91100958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glucosyltransferase N - Streptococcus salivarius (fragment)
C; Species: Streptococcus salivarius
C; Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
                                                                          glucosyltransferase - Streptococcus salivarius C;Species: Streptococcus salivarius C;Date: 22-Oct-1999 #sequence_revision 22-Oct-
                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M29296
C;Superfamily: cpl repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Streptococcus mutans
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, February 1998 A;Description: Streptococcus salivarius V1477 gtf. A;Reference number: 220854
                                                             C; Accession:
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A;Molecule type: DNA
A;Residues: 1-1431 <HON>
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A; Title: Streptococcus salivarius ATCC 25975
A; Reference number: Z20909; MUID: 95122197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
                                             R; Simpson, C.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:AF049609; NID:g2935545; PID:g2935546; PIDN:AAC05156.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-1449 <JAF>
                                Infect. Immun. 63, 609-621, 1995
                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 13
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Matches
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13; Conservative
                                                                T30858
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                                             Giffard, P.M.; Jacques, N.A.
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59.1%;
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No.
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             two genes
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A;Cross-references:
C;Genetics:
A;Gene: gtfm
A; Experimental source: clone C; Genetics:
A; Gene: end-1; F58E10.2
A; Map position: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:L34406
C;Superfamily: cpl repeat homology
F;173-192/Domain: cpl repeat homology <CPl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detranase inhibitor precursor - Streptococcus sobrinus (strain UAB66, serotype g)
C;Species: Streptococcus sobrinus
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: T30858
A; Status: preliminary; t:
A; Molecule type: DNA
A; Residues: 1-1577 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                 GATA transcription factor end-1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Deceles: Caenorhabditis elegans C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000 C;Accession: T37244; T22912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
A55221
                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-221 <WIL>
                                                                                                                                                    A;Reference number:
                                                                                                                                                                      A; Reference number: Z19637
                                                                                                                                                                                                                                                                                                                         R; Zhu, J.; Hill, R.J.; Heid, P.J.; Fukuyama, M.; Sugimoto, A.; Genes Dev. 11, 2883-2896, 1997
A;Title: End-1 encodes an apparent GATA factor that specifies A;Reference number: Z21642; MUID:98019168
                                                                          A; Cross-references:
                                                                                                                                                                                                             R;McMurray, A.
                                                                                                                                                                                                                                                                                                   A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
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A; Residues: 1-329 <SUN>
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                                                                                                                                                                                                                             A;Cross-references:
                                                                                                                                                                                                                                                A;Residues: 1-221 <ZHU>
                                                                                                                                                                                                                                                                      A;Molecule
                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local S
Matches 15
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15; Conser
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                                                                            EMBL: 281555;
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                                                                                                                                                                                        Library,
                                                                                                                                                                                                                                                                                                                                                                                P.J.; Fukuyama, M.; Sugimoto, A.;
                                                          F58E10
                                                                          PIDN:CAB04513.1; GSPDB:GN00023;
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Pred. No.
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Pred. No. 0.0044;
1; Mismatches 5;
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                                                                                                                                                                                                                             NID:g2655205; PIDN:AAB97516.1;
                                                                                                                                                                                           November 1996
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                                                                                                                                                                                                                                                                                                                                            the endoderm precursor
                                                                                                                                                                                                                                                                                                                                                                                  Priess, J.R.;
                                                                            CESP: F58E10.2
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A:Introns: 71/1; 128/3; 162/2
C:PRONETION: Involved in the specification of germ layer and founder cell identity A:Description: involved in the specification of germ layer and founder cell identity C:Reywords: transcription factor; zinc finger

QUEYWARCH 48.2% Score 54; DB 2; Length 221;
Best Local Similarity 57.9%; Pred: No. 0.23;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 TGARTINGOLLYRANGVQ 19
Db 156 SGAIDCNGCSLYFRKNGIQ 174

Search completed: March 27, 2002, 14:01:17
Job time: 479 sec
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Maximum DB seq length: 2000000000
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               Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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119
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2: /cgn2_6/ptcdata/2/paa/US089_COMB.pep: *
2: /cgn2_6/ptcdata/2/paa/US089_COMB.pep: *
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(cgn2_6/ptcdata/2/paa/US094_COMB.pep: *
(cgn2_6/ptcdata/2/paa/US095_COMB.pep: *
(cgn2_6/ptcdata/2/paa/US096_COMB.pep: *
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Copyright (c) 1993 - 2000 Comp
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/paa/US06_COMB.pep:*
/cgn2_6/ptodata/2/paa/US07_COMB.pep:*
/cgn2_6/ptodata/2/paa/US080_COMB.pep:*
/cgn2_6/ptodata/2/paa/US081_COMB.pep:*
/cgn2_6/ptodata/2/paa/US081_COMB.pep:*
/cgn2_6/ptodata/2/paa/US082_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/2/paa/US083_COMB.pep:*
/cgn2_6/ptodata/2/paa/US084_COMB.pep:*
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5.116 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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		æ				
Result		Query				
No.	Score	Match	Match Length DB	DB	ID	Description
1	119	100.0	21		US-09-290-049-1	Sequence 1, Appli
2	- 119	100.0	21	16	US-09-290-049-10	Sequence 10, Appl
ω	119	100.0	1475		US-09-557-848-2	Sequence 2, Appli
4	119	100.0	1475		US-09-740-274-2	Sequence 2, Appli
G	110	92.4	1375		US-09-740-274-4	Sequence 4, Appli
6	108	90.8	21		US-09-290-049-12	Sequence 12, Appl
7	108	90.8	21		US-09-290-049-14	Sequence 14, Appl
8	75	63.0	21		US-09-290-049-11	Sequence 11, Appl
9	75	63.0	1430	20	US-09-649-885-2	Sequence 2, Appli

35 35 35 36 36 36 36 36 36 36 36 36 36 36 36 36	331 329 8 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	10 11 12 13 14 15 16 17 18
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38.7 38.7 38.7 38.7 38.7 38.7 38.7 37.8		50.3 50.3 50.3 50.3 42.0 42.0 42.0 42.0 60.3
336 336 394 476 476 2596 2603 185 194	534 196 220 539 539 539 1198 279	1430 2057 2057 306 340 546 549 549 391 401
115 121 122 124 124 124 124 124 15	124 24 24 24 24 21 11 11 11 11 11 11 11 11 11 11 11 11	21 16 19 19 19 19 24 24 24 24
US-09-198 452A-662 US-09-438-185-626 US-09-739-449-8822 US-09-803-110-8822 US-09-803-110-8822 PCT-US01-22636-9 US-09-252-991A-21255 US-60-215-161-7203 US-60-215-161-5891	US-09-344-882-24 US-60-324-109-33149 US-60-324-109-33149 US-60-259-52-2413-164 US-60-229-518-331 US-60-229-518-331 US-60-229-518-331 US-60-229-518-331 US-60-229-518-331 US-60-229-518-331 US-09-764-875-762 US-09-764-875-762 US-09-417-507-26597 PCT-US01-08656-5595 US-09-673-395A-221 US-09-673-395A-221 US-09-673-395A-221 US-09-538-092-348-71	274-6 049-13 203-2 203-2 298A-660 298A-660 109-1701 109-1678 1109-2073 3109-207796-2257
6626, 626, 8822, 8822, 9, Apr 9, Apr 9, Apr 2125; 7203, 7203, 5891, 5719, 9825, 80, 1	sequence 24, Appl Sequence 31149, A Sequence 33149, A Sequence 164, App Sequence 164, App Sequence 164, App Sequence 75, App Sequence 762, App Sequence 762, App Sequence 5595, Ap Sequence 5595, Ap Sequence 221, App Sequence 248, App Sequence 348, App	6, Ap 13, Ap 2, Ap 661, 660, 17015 16789 20736 222, Ap 2227, Ap

## ALIGNMENTS

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RESULT 1

US-09-290-049-1

Sequence 1, Application US/09290049

Sequence 1, Application US/09290049

Sequence 1, Application US/09290049

Sequence 1, Application US/09290049

APPLICANT: Smith, Daniel J.

APPLICANT: Taubman, Martin A.

TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL

TITLE OF INVENTION: ARITIN A.

TITLE OF INVENTION: ARITIN A.

TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL

TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES

FILE APPLICATION

TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES

FILE APPLICATION

TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES

FEATLIER FILING DATE: 1999-01-08

SERVICE APPLICATION

TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES

FEATLIER FILING DATE: 1999-01-08

SERVICE APPLICATION

TOMBER OF SOLUTION

TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES

FOUNDATION

TITLE OF INVENTION

TITLE OF
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В

ANDHLSILEAWSDNDTPYLHD

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TITLE OF INVENTION: Substitutes for modified Starch and TITLE OF INVENTION: Latexes in Paper Manufacture FILE REFERENCE: 0356D2

CURRENT APPLICATION NUMBER: US/09/557,848

CURRENT FILING DATE: 2000-04-26

CARLIER APPLICATION NUMBER: 08/478,704

ARLIER FILING DATE: 1995-06-07

EARLIER FILING DATE: 1995-06-07

EARLIER FILING DATE: 1998-01-16

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Smith, Daniel J.

APPLICANT: Taubman, Martin A.

ITITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL

ITITLE OF INVENTION: CARIES

FILE REFERENCE: FDC98-0192A

CURRENT APPLICATION NUMBER: US/09/290,049

CURRENT TILING DATE: 1999-04-12

EARLIER APPLICATION NUMBER: 60/081,550

EARLIER APPLICATION NUMBER: 60/15,142

EARLIER APPLICATION NUMBER: 60/115,142

EARLIER APPLICATION NUMBER: 50/115,142

EARLIER FILING DATE: 1999-01-08

NUMBER OF SEQ ID NOS: 19

SOSTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 10

LENCTH: 21

TYPE: PRT

COCANICM: S muttans
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                                                                US-09-740-274-2
                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Streptococcus mutans US-09-557-848-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-09-557-848-2
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                                                                                    RESULT
                      Sequence 2, Application US/09740274 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09557848 GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 21; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/09290049 GENERAL INFORMATION:
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
  APPLICANT:
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                                                                                                                                                     481 ANDHLSILEAWSDNDTPYLHD 501
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1 ANDHLSILEAWSDNDTPYLHD 21
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Nichols, Scott E.
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Pred. No. 5.2e-09;
); Mismatches 0;
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Pred. No. 5.3e-11;
; Mismatches 0;
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                            Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                 SOFTWARE:
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09740274
                                                                                                                                                                                                                                                                  PRIOR EILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 09/008,172
PRIOR FILING PAGE
                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1995-(PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/740,274
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 09/210,361
PRIOR FILING DATE: 1998-12-11
                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1998-PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-
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TITLE OF INVENTION: Glucan-containing Compositions and Paper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
TYPE: PR
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PRIOR
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PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 08/
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CURRENT FILING DATE: 2000-12-19
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                                                                                                                                                                                                                                  PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE:
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                                                                                                                                                                LENGTH: 1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ANDHLSILEAWSDNDTPYLHD 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 09/009,620
FILING DATE: 1998-01-20
APPLICATION NUMBER: 08/485,243
FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .: 1475
PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 09/0
FILING DATE: 1998-01-16
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                                 Conservative
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1995-06-07
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                                               92.4%;
95.2%;
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                                                                                                                                                                                                                                              08/482,711
                                0;
                                             Score 110; DB 21
Pred. No. 1.2e-07
                                 Mismatches
                                                                Length 1375;
                                 Indels
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507 ANDHLSILEAWSYNDTPYLHD 527

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APPLICANT: Smith, Daniel J.

APPLICANT: Tabbman, Martin A.

ITITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL

TITLE OF INVENTION: CARIES

FILE REFERENCE: FDC98-01p2A

CURRENT APPLICATION NUMBER: US/09/290,049

CURRENT FILING DATE: 1999-04-12

EARLIER APPLICATION NUMBER: 60/081,550

EARLIER FILING DATE: 1998-04-13

EARLIER FILING DATE: 1998-04-13

EARLIER FILING DATE: 1998-04-13

EARLIER FILING DATE: 1999-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: SVATHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARIES
FILE REFERENCE: FDC98-01.D2A
CURRENT APPLICATION NUMBER: US/09/290,049
CURRENT FILING DATE: 1999-04-12
EARLIER APPLICATION NUMBER: 60/081,550
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/115,142
EARLIER FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 19
NUMBER OF SEQ ID NOS: 19
RESULT 8
US-09-290-049-11
; Sequence 11, Application US/09290049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-290-049-14
; Sequence 14, Application US/09290049
; GENERAL INFORMATION:
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; ORGANISM: S.
US-09-290-049-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-290-049-12
                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 14
LENGTH: 21
                                                                                                                                                                                      Matches
                                                                                                                                                                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OFTWARE: FastSEQ for Windows Version 3.0
Q ID NO 12
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 85. hes 18; Conservative
                                                                                                                                                                                    Local Similarity
nes 18; Conserv
                                                                                                       1 ANDHLSILEAWSDNDTPYLHD 21
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1 ANNHVSIVEAWSDNDTPYLHD 21
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85.7%;
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85.7%;
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Pred. No. 2.76
3; Mismatches
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Pred. No. 2.7e-09;
3; Mismatches 0;
                                                                                                                                                                                    DB 16;
2.7e-09;
nes 0;
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GENERAL INFORMATION:

APPLICANT: Smith, Daniel J.

APPLICANT: Taubman, Martin A.

TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL

TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL

TITLE OF INVENTION: CARIES

FILE REFERENCE: FDC98-01p2A

CURRENT APPLICATION NUMBER: US/09/290,049

CURRENT FILING DATE: 1999-04-12

EARLIER APPLICATION NUMBER: 60/01,550

EEARLIER FILING DATE: 1998-04-13

EARLIER FILING DATE: 1998-01-08

EARLIER APPLICATION NUMBER: 60/115,142

EARLIER FILING DATE: 1999-01-08
                                                                                                                                 RESULT 10
US-09-740-274-6
; Sequence 6, Application US/09740274
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09649885
GENERAL INFORMATION:
APPLICANT: Nichols, Scott E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
CURRENT APPLICATION NUMBER: US/09/740,274
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 09/210,361
PRIOR FILING DATE: 1998-12-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/649,885
CURRENT FILING DATE: 2000-08-28
PRIOR APPLICATION NUMBER: US 09/008,172
PRIOR FILING DATE: 1998-01-16
PRIOR FILING DATE: 1998-01-16
                                                                                             APPLICANT: Nichols, Scott E.
TITLE OF INVENTION: Glucan-containing Compositions
                                                                                FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR EPPLICATION NUMBER: 08/482,711 PRIOR FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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TYPE: PRT
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71.4%;
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Pred. No. 0.034;
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Pred. No. 0.00036;
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PRIOR APPLICATION NUMBER: 08/PRIOR FILING DATE: 1995-06-07

08/478,704 09/007,999

APPLICATION NUMBER: 09/0

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PRIOR FILING DATE: 1997/005, 2007
PRIOR APPLICATION NUMBER: 09/005, 2007
PRIOR FILING DATE: 1998-01-20
PRIOR PRIOR PLICATION NUMBER: 09/485, 243
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 09/008, 172
PRIOR APPLICATION NUMBER: 09/482, 711
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US-09-290-049-13
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US-09-290-049-13
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CURRENT APPLICATION NUMBER: US/09/290,049
CURRENT FILING DATE: 1999-04-12
EARLIER APPLICATION NUMBER: 60/081,550
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/115,142
EARLIER FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 19
                                                                                                            Sequence 2, Application US/09499203 GENERAL INFORMATION:
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Best Local
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Best Local Similarity
APPLICANT: WELSH, Thomas
APPLICANT: QUANZ, Martin
APPLICANT: KNUTH, Karola
TITLE OF INVENTION: Nucleic Acid Molecules
FILE REFERENCE: 147-196P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: SYMPHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARIES
                                                                                           APPLICANT: KOSSMANN, Jens
                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 3.0
Q ID NO 13
LENGTH: 21
TYPE: PRT
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TYPE: PRT
ORGANISM: streptococcus mutans
09-740-274-6
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NUMBER OF SEQ ID NOS:
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71.4%;
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Pred. No.
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                  Encoding Alternansucrase
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                                                                                                                                                               Sequence 660, Application US/09595298A
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: BROVER, Vyacheslav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/595,298A
CURRENT FILING DATE: 2000-66-16
NUMBER OF SEQ ID NOS: 2756
SOFTWARE: Patentin version 3.0
SEQ ID NO 661
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Best Local Similarity
Matches 9; Conserv
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                                 SEQ ID NO 660
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                                                                                                            TITLE OF INVENTION: Sequence TITLE OF INVENTION: Thereby TITLE OF INVENTION: 2750-0953P
                                               FILE REFERENCE: 2750-0953P
CURRENT APPLICATION NUMBER: US/09/595,298A
CURRENT FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 2756
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BROVER, Vyacheslav TITLE OF INVENTION: Sequence TITLE OF INVENTION: Thereby
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CURRENT FILING DATE: 2000-02-08
NUMBER OF SEQ ID NOS: 54
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LENGTH: 34
TYPE: PRT
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OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: peptide
LOCATION: (1)..(306)
OTHER INFORMATION: Ceres
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DYEQIMEAWSDKGTLYV 216
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55.0%;
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52.9%;
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Pred. No. 49;
3; Mismatches
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49;
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ORGANISM: Arabidopsis Thaliana

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; NUMBER OF SEQ ID NOS: 33196
; SEQ ID NO 17015
; LENGTH: 546
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
US-60-324-109-17015
                                                                                                                                                                                                                                                                                                                                                                                                    Q-324-109-17015
Quence 17015, Application US/60324109

"SENERAL INFORMATION:

APPLICANT: Cao, Yongwei
APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.

APPLICANT: Kovalic, David K.

APPLICANT: Liu, Jingdong
APPLICANT: Stein, Joshua
TITILE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)B
CURRENT APPLICATION NUMBER: US/60/324,109
CURRENT FILING DATE: 2001-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: peptide; LOCATION: (1)..(340); OTHER INFORMATION: Ceres Seq. ID no. 1026740; NAME/KEY: misc_feature; LOCATION: ()..(); OTHER INFORMATION: Xaa is any aa, unknown or other US-09-595-298A-660
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Search completed: March 27, 2002, 14:20:22 Job time: 1569 sec
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Best Local Similarity 52.9%;
Matches 9; Conservative
                                                                                                                                                                       Query Match 41.6%;
Best Local Similarity 58.8%;
Matches 10; Conservative
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                                                                                              144 NDELAALETW-DNGKPY 159
                                                                                                                  2 NDHLSILEAWSDNDTPY 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 DHLSILEAWSDNDTPYL 19
                                                                                                                                                                       Score 49.5; DB 24;
Pred. No. 1.1e+02;
1; Mismatches 5;
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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   length: 0
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Match
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   Issued_Patents_AA:*

| /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
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| /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
| /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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| /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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US-08-361-920-23
US-08-483-432-23
US-08-483-432-23
US-08-48-43-2
US-08-596-291-3
US-09-100-804-3
US-09-100-805-31-2
US-09-290-640-46
US-08-277-231A-3
US-08-277-231A-3
US-08-277-2326-6
US-08-277-255-12
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US-08-333-7500-5
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US-08-333-7500-5
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Sequence 2
Sequence 3
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 EARLIER FILING DATE: 1995-06-07
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US-09-210-361-? US-09-210-361-? Sequence 2, hpplication US/09210361 Patent No. 5284479 GENERAL INFORMATION: Scott E. APPLICANT: N.CENOLS, SCOTT E. TITLE OF INVENTION: Substitutes for Modified Starches and TITLE OF INVENTION: Latexes in Paper Manufacture FILE REFERRICE: 0357CR CURRENT APPLICATION NUMBER: US/09/210,361 CURRENT FILING DATE: 1998-12-11 FEARLIER APPLICATION NUMBER: 09/007,999 EARLIER FILING DATE: 1998-01-16 EARLIER FILING DATE: 1998-01-6-07 EARLIER APPLICATION NUMBER: 08/478,704	Query Match 100.0%; Score 119; DB 3: Length 1475; Best Local Similarity 100.0%; Pred. No. 6.4e-11; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps Qy 1 ANDH75:SAWSDNDTPYLHD 21	RESULT 1 US-09-07-999-2 Sequence 2, Application US/09007999 Patent No. 6087559 GENERAL INFORMATION: SUBSTITUTE OF INVENTION: Substitutes for Modified Starch and TITLE OF INVENTION: Latexes in Paper Manufacture FILE REFERENCE: 0356D CURRENT APPLICATION NUMBER: US/09/007,999 CURRENT ETLING DATE: 1998-01-16 EARLIER APPLICATION NUMBER: 08/478,704 EARLIER FILING DATE: 1998-06-07 NUMBER OF SEQ ID NOS: 2 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 2 LENGTH: 1475 TYPE: PRT US-09-007-999-3	28 40 33.6 839 4 US-09-197-636-2 Sequence 2, Appli 30 40 33.6 839 4 US-09-197-636-8 Sequence 4, Appli 31 40 33.6 839 4 US-09-197-636-8 Sequence 8, Appli 31 40 33.6 2860 2 US-08-826-265-2 Sequence 2, Appli 32 40 33.6 3898 4 US-09-750-717-2 Sequence 2, Appli 33.5 33.2 567 1 US-08-258-261B-4 Sequence 2, Appli 35 39.5 33.2 567 1 US-08-456-837-4 Sequence 4, Appli 39.5 33.2 567 1 US-08-457-342-4 Sequence 4, Appli 39.5 33.2 567 1 US-08-457-342-4 Sequence 4, Appli 39.5 33.2 567 1 US-08-457-342-4 Sequence 4, Appli 39.5 33.2 567 1 US-08-457-345A-4 Sequence 4, Appli 39.5 33.2 567 1 US-08-457-35A-4 Sequence 4, Appli 39.5 33.2 567 1 US-08-459-214-4 Sequence 4, Appli 39.5 33.2 567 1 US-08-459-214-4 Sequence 4, Appli 39.5 33.2 567 2 US-08-79-214-4 Sequence 4, Appli 39.5 33.2 567 3 US-09-028-934-4 Sequence 4, Appli 39.5 33.2 567 3 US-09-028-934-4 Sequence 4, Appli 39.5 33.2 567 3 US-09-028-934-4 Sequence 2, Appli 39.5 33.2 567 3 US-09-369-618-2 Sequence 2, Appli 39.5 39.5 39.5 30.5 30.5 30.5 30.5 30.5 30.5 30.5 30

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; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-09-210-361-2
                                                                                                                                                 RESULT 4
US-09-008-172-2

; ORGANISM: streptococcus mutans
US-09-210-361-4
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US-09-210-361-4
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EARLIER APPLICATION NUMBER: 09/007,999

EARLIER FILING DATE: 1998-01-16

EARLIER FILING DATE: 1998-01-16

EARLIER FILING DATE: 1995-06-07

EARLIER FILING DATE: 1995-06-07

EARLIER FILING DATE: 1998-01-20

EARLIER FILING DATE: 1998-01-20

EARLIER FILING DATE: 1998-01-20

EARLIER FILING DATE: 1998-01-20
                                                                                                           Sequence 2, Application US/09008172 Patent No. 6127602
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Best Local Similarity
                                                                                        GENERAL INFORMATION:
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Best Local :
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                   FILE
                           APPLICANT: Nichols, Scott E.
TITLE OF INVENTION: Substitutes for Modified Starch
TITLE OF INVENTION: Latexes in Paper Manufacture
 CURRENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: 08/485,243
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 09/008,172
EARLIER FILING DATE: 1998-01-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Substitutes for Modified Starches and TITLE OF INVENTION: Latexes in Paper Manufacture
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SOFTWARE: FastSEQ for Windows Version
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EARLIER FILING DATE: 1998-01-16
EARLIER APPLICATION NUMBER: 08/482,711
EARLIER FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQ ID NO 4
LENGTH: 1375
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                   REFERENCE:
                                                                                                                                                                                                                                                 1 ANDHLSILEAWSDNDTPYLHD 21
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APPLICATION NUMBER: US/09/008,172
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95.2%;
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Pred. No. 1.7e-09;
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Pred. No. 6.4e-11;
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RESULT 6
US-08-793-824-2
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; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-09-008-172-2
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                 GENERAL INFORMATION:
APPLICANT: Simpson,
APPLICANT: Giffard,
APPLICANT: Jacques,
TITLE OF INVENTION:
TITLE OF INVENTION:
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
LENGTH: 1430
                                                                                                                   Sequence 2, Application Patent No. 5981838
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Best Local Similarity
Matches 15; Conserv
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EARLIER FILING DATE: 1995-06-07
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 09/008,172
EARLIER FILING DATE: 1998-01-16
EARLIER FILING DATE: 1998-01-17
EARLIER FILING DATE: 1995-06-07
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EARLIER APPLICATION NUMBER: 08/482,711
EARLIER FILING DATE: 1995-06-07
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CURRENT FILING DATE: 1998-12-11
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     NUMBER OF SEQUENCES
                                                                                                                                                                                                                        495 AINHLSILEAWSDNDPQYNKD
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o. 6284479
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                                                                Simpson,
Giffard,
                                                  Jacques,
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71.4%;
               , Philip Morrison
, Nicholas Anthony
Genetic Manipulation o
Increase Stored Carboh
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Increase
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71.4%;
                                                                                   Christine Lynn
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Pred. No. 0.00084;
1; Mismatches 5
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                   Carbohydrates
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                                    of Plants
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CORRESPONDENCE ADDRESS:

ADDRESSEE: Griffith

Hack & Co

STREET: CITY: STATE:

Australia

Level 8, 168 Walker Street
No. 5981838th Sydney
New South Wales

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                                                                                                                                                                                                                                                                                                                                            Patent No. 5457046
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Woeldike, Helle F.
APPLICANT: Hagen, Frederick
APPLICANT: Hjort, Carsten M.
APPLICANT: Sven, Hastrup
TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
TITLE OF INVENTION: or Hemicellulose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 23, Application US/08361920 Patent No. 5457046
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Best Local
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                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 54570460 No. 5457046disk of No. ADDRESSEE: No. 54570460 Avenue, 62nd Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 61 2 9957 5944
TELEFAX: 61 2 957 6288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1577 amino acids
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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nes 13; Conserv
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CLASSIFICATION:
                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                     CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/793,824
                    CLASSIFICATION:
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72.2%;
                                                        US/08/361,920
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Pred. No. 0.08
0; Mismatches
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0.084;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: (FILING DATE: 22-DEC-1
APPLICATION NUMBER: (
                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATION OPERATING SYSTEM: PC-DO SOFTWARE: PATENTIN Relaction DATA:
                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 385 amino acid
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         ATTORNEY/AGENT INFORMATION:
                                            PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                329 ANDYLTVMNACLAVPKCVGITVWGVSDKDSWRPGDNPLLYD 369
                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 07-JUN
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FILING DATE: 08-MAY-1991
                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                        CLASSIFICATION:
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                                                                             FILING DATE:
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New York
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Hjort, Carsten M
Sven, Hastrup
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                                                                                                                                                                                                                                                                 IBM PC compatible SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                             No.
                                                                                                                                                                                                   UMBER: US/08/479,939
07-JUN-1995
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                               08-MAY-1993
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Elias
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24.4%;
                                                                                          DK 1158/90
                                            PCT/DK91/00124
                                                                                                                       US 07/940,860
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Pred. No.
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13;
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US-08-483-432-23

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; Patent No. 5763254
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                         APPLICATION NUMBER: US 07/940,860
FILING DATE: 28-OCT-1992
APPLICATION NUMBER: DK 1158/90
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK91/00124
FILING DATE: 08-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
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                                                                                            TELEFAX: 212-867-0298 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,432
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
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LENGTH: 385 amino acids
MOLECULE TYPE:
                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                            TELEPHONE: 212-867-0298
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                   TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
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405 Lexington Avenue, 62nd Floor
                                                     385 amino acids
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Hjort, Carsten M.
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protein
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Pred. No. 13;
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CURRENT APPLICATION NUMBER: US/09/311,170
CURRENT FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 384
Type: nor
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Best Local Similarity
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Best Local Similarity
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          CLASSIFIATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
                                                                                                               COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: HELDIN, CARL-HEBRIK
TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCE
TITLE OF INVENTION: TYROSINE PHOSPHATASES
                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GRE
ATTORNEY/AGENT INFORMATION:
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                                                                              APPLICATION NUMBER: US/08/596,291 FILING DATE: 09-AUG-1996
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SARAS,
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JAN
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Pred. No. 19;
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Pred. No. 13;
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US-09-100-804-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                        APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09943
FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617/720-2441
TELEX: 92-1742 EZEKIEL
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                     INFORMATION FOR SEQ ID NO: 3:
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REFERENCE/DOCKET NUMBER: LO-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
LENGTH: 2465 amino aci
                                                                                               NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: LO4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: GONEZ, LEONEL JORGE
APPLICANT: SARAS, JAN
APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: HELDIN, CARL-HENRIK
TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
TITLE OF INVENTION: *EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2347 HISHLNFTAWPDHDTP 2362
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                                                        TELEPHONE: 01, TELEPHONE: 617-720-2441
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nes 9; Conserv
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TYPE: amino acid
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Pred. No. 2.5e+0;
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PCT-US94-09943-2
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 2466
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GENERAL INFORMATION:
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Best Local :
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Best Local
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APPLICANT: Heldin, Carl-Henrik
TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1
FILE REFERENCE: L0461/7030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/080,855A CURRENT FILING DATE: 1998-05-18
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APPLICANT: Franzn, Petra
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                                                                                                                                                               TITLE OF INVENTION: P
TITLE OF INVENTION: E
TITLE OF INVENTION: T
NUMBER OF SEQUENCES:
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             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                       2348 HISHLNFTAWPDHDTP 2363
                                                                                                                                 CORRESPONDENCE ADDRESS:
STREET: 600 ATLANTIC AVENUE
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TOPOLOGY: linear
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les 9; Conserv
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                                                                                                                    BOSTON
                                                                                                                                                                                                                                                                                                                                   Application PC/TUS9409943
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Hellman, Uli
                                                                                                MASSACHUSETTS
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                                                                                   USA
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PatentIn Release #1.0, Version #1.25
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56.2%;
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56.2%;
                                                                                                                                                                                                 PRIMARY STRUCTURE AND FUNCTIONAL EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
                                                                                                                                                                                  TYROSINE PHOSPHATASES
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Pred. No.
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Pred. No.
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CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/115,573
FILING DATE: 01-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: TWOMEY, MICHAEL J.
REGISTRATION NUMBER: P-38,349
REFERENCE/DOCKET NUMBER: LO461/7000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEPHONE: 617/720-3500
TELEX: 92-1742 EZEKIEL
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARCTENISTICS:
LENGTH: 2466 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: protein
PCT-US94-09943-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-09-290-640-46
US-09-290-640-46; Sequence 46, Application US/09290640; Patent No. 6204055; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                    APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-0351
CURRENT APPLICATION NUMBER: US/09/290,640
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin Ver. 2.0
FEQ ID NO 46
EQ ID NO 46
TYPE: PRT
ORGANISM: Homo sapiens
US-09-290-640-46
Search completed: March 27, 2002, 13:59:26 Job time: 579 sec
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Best Local Similarity 56.2%;
Matches 9; Conservative
                                                                                             CÜRRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09943
FILING DATE: 01-SEP-1994
CLASSIFICATION:
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Result
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5: /cgn2_6/ptodata/1/paa/U

6: /cgn2_6/ptodata/1/paa/U

7: /cgn2_6/ptodata/1/paa/U

8: /cgn2_6/ptodata/1/paa/U
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	Sequence 10188, A	Sequence 10188, A	Sequence 10188, A	Sequence 11634, A	Sequence 11634, A	Sequence 11634, A	Sequence 42525, A	•	Sequence 25321, A	Sequence 25322, A	Sequence 80, Appl	Sequence 5719, Ap	Sequence 5891, Ap	Sequence 7203, Ap	Sequence 2226, Ap	Sequence 73, Appl	27414,	Sequence 27415, A	Sequence 27416, A	Sequence 90, Appl

## ALIGNMENTS

US-09-562-328-20

Sequence 20, Application US/09562328 GENERAL INFORMATION:

APPLICANT: LESS, ANDREW
APPLICANT: TAUBMAN, MARTIN A.
APPLICANT: TAUBMAN, MARTIN A.
APPLICANT: SMITH, DANIEL J.
TITLE OF INVENTION: CONJUGATE VACCINES FOR THE PREVENTION OF DENTAL CARIES
FILE REFERENCE: 04995.0046-01
CURRENT FILING DATE: 10900-05-01
PRIOR APPLICATION NUMBER: 09/288,965
PRIOR APPLICATION NUMBER: 09/288,965
PRIOR APPLICATION NUMBER: 09/288,965
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 20

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APPLICANT: Smith, Daniel J.
APPLICANT: Tabbman, Martin A.
APPLICANT: Tabbman, Martin A.
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FO)
TITLE OF INVENTION: CARIES
FILE REFERENCE: 1564.1008-002
CURRENT APPLICATION NUMBER: US/09/290,049A
CURRENT FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR FILING DATE: 1998-04-13
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 19
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; TYPE: PRT
; ORGANISM: Streptococcus
US-09-562-328-20
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US-09-290-049A-1
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SOFTWARE: FastSEQ for Windows Version
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Pred. No. 2.9e-12;
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SEQ ID NO 1 LENGTH: 21

TYPE: PRT

FEATURE:

ORGANISM: Artificial Sequence

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; TYPE: PRT ; ORGANISM: Streptococcus sp US-09-562-328-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 1564.1008-002
CURRENT APPLICATION NUMBER: US/09/290,049A
CURRENT FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 60/081.550
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEO ID NOS: 19
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                                                                                                                                                                                                    Sequence 21, Application US/09562328
GENERAL INFORMATION:
APPLICANT: LEES, ANDREW
APPLICANT: TAUBMAN, MARTIN A.
APPLICANT: SMITH, DANIEL J.
TITLE OF INVENTION: CONJUGATE VACCINES FOR THE
FILE REFERENCE: 04995.0046-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 10 LENGTH: 21
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                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/562,328
CURRENT FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 09/288,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Smith, Daniel J.
APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES
TITLE OF INVENTION: CARIES
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                                                                                                             PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 44
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100.0%; Pred. No. 2.9e-12;
tive 0; Mismatches 0;
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Pred. No. 2.9e-12;
Mismatches 0;
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RESULT 7 US-09-290-049A-12

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; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 23

; LENGTH: 21

; TYPE: PRT

; ORGANISM: Streptococcus sp.

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                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/288,965
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATENTIN VEr. 2.1
SEQ ID NO 25
LENGTH: 21
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                APPLICANT: TAUBMAN, MARTIN A.
APPLICANT: SMITH, DANIEL J.
TITLE OF INVENTION: CONJUGATE VACCINES FOR THE PREVENTION OF DENTAL CARIES
FILE REFERENCE: 04995.0046-01
CURRENT APPLICATION NUMBER: US/09/562,328
CCURRENT FILING DATE: 2000-05-01
CCURRENT FILING DATE: 2000-05-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/288,965
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 44
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CURRENT FILING DATE: 2000-05-01
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APPLICANT: SMITH, DANIEL J.
TITLE OF INVENTION: CONJUGATE VACCINES FOR THE PREVENTION OF DENTAL CARIES
FILE REFERENCE: 04995.0046-01
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                                                                                                                                                                                       TYPE: PRT
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Sequence 12, Application US/09290049A GENERAL INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 21
TYPE: PRT
ORGANISM: S. sobrinus
                                                                                                       Sequence 22, Application US/09562328 GENERAL INFORMATION:
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LENGTH: 21
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Best Local
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TITLE OF INVENTION: SYNYHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARIES
FILE REFERENCE: 1564.1008-002
CURRENT APPLICATION NUMBER: US/09/290,049A
CURRENT FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR FILING DATE: 1998-04-13
PRIOR FILING DATE: 1998-04-13
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TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL
TITLE OF INVENTION: CARIES
FILE REFERENCE: 1564.1008-002
CURRENT APPLICATION NUMBER: US/09/290,049A
CURRENT FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR APPLICATION NUMBER: 60/115,142
PRIOR FILING DATE: 1999-01-08
                                           APPLICANT: LEES, ANDREW APPLICANT: TAUBMAN, MAI APPLICANT: SMITH, DANII
APPLICANT: TAUBMAN, MARTIN A.
APPLICANT: SMITH, DANIEL J.
TITLE OF INVENTION: CONJUGATE VACCINES FOR THE PREVENTION OF DENTAL CARIES
FILE REFERENCE: 04995.0046-01
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SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                                                      90.8%;
Local Similarity 85.7%;
nes 18; Conservation
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1 ANNHVSIVEAWSDNDTPYLHD 21
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Pred. No. 1.5e-10;
3; Mismatches 0
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; SEQ ID NO 22
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Streptococcus sp.
US-09-562-328-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 21
TYPE: PRT
ORGANISM: S. mutans
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 545
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Best Local Similarity 71.4%;
Matches 15; Conservative
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Best Local Similarity 71.4
Matches 15; Conservative
                                                                             APPLICANT: RAHAOUI, HAKIM
APPLICANT: LEER, ROBERT-JAN
TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASE AND NOVEL GLUCAN
FILE REFERENCE: BO 43388
CURRENT APPLICATION NUMBER: US/09/604,957
CURRENT FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 00201871.1
PRIOR FILING DATE: 2000-05-25
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TITLE OF INVENTION: CARIES
FILE REFERENCE: 1564.1008-002
CURRENT APPLICATION NUMBER: US/09/290,049A
CURRENT APPLICATION NUMBER: US/09/290,049A
PRIOR APPLICATION NUMBER: 50/081,550
PRIOR APPLICATION NUMBER: 60/081,550
PRIOR PILING DATE: 1998-04-13
PRIOR FILING DATE: 1998-04-13
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APPLICANT: DIJKHUIZEN, LUBBERT
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CURRENT FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 09/288,965
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 44
                                                                PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 17
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71.4%;
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Pred. No. 2.3e-05;
1; Mismatches 5
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Pred. No. 2.3e-05;
1; Mismatches 5
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Sequence 24, Application US/09562328

GENERAL INFORMATION:

APPLICANT: LEES, ANDREW
APPLICANT: LEES, ANDREW
APPLICANT: TAUBMAN, MARTIN A.

APPLICANT: SMITH, DANIEL J.

TITLE OF INVENTION: CONJUGATE VACCINES FOR THE PREVENTION OF DENTAL CARIES
FILE REFERENCE: 04995.0046-01

CURRENT FILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: US/09/562,328

CURRENT FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

INVESER OF SEQ ID NOS: 44

SOSTWARE: PATENTIN Ver. 2.1

TYPE: DET
                                                                                                               APPLICANT: SMITH, Daniel J.

APPLICANT: Tauboman, Martin A.

TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR DENTAL

TITLE OF INVENTION: CARIES

FILE REFERENCE: 1564.1008-002

CURRENT APPLICATION NUMBER: US/09/290,049A

CURRENT FILING DATE: 1999-04-12

PRIOR APPLICATION NUMBER: 60/081,550

PRIOR APPLICATION NUMBER: 60/15,142

PRIOR APPLICATION NUMBER: 60/115,142

PRIOR FILING DATE: 1999-01-08

NUMBER OF SEQ ID NOS: 19

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13

LENGTH: 21

TYPE: PRT
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                                                                                           ; ORGANISM: S. downei
US-09-290-049A-13
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Best Local Similarity
Matches 14; Conserv
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Best Local Similarity 71.4
Matches 15; Conservative
                  Query Match
Best Local Similarity
   Matches
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equence 13, Application US/09290049A
ENERAL INFORMATION:
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73.7%;
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73.7%;
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Pred. No. 4.7e-05;
                Score 73; DB 6;
Pred. No. 4.7e-05;
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Pred. No. 0.
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PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 523
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SOFTWARE: PatentIn Ver. 2.1
SEQ_ID_NO_6.
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Best Local Similarity
Matches 14; Conserv
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/604,957
CURRENT FILING DATE: 2000-06-28
                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/604,957
CURRENT FILING DATE: 2000-06-28
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TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASE AND NOVEL GLUCAN
FILE REFERENCE: BO 43388
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APPLICANT: DIJKHUIZEN, LUBBERT
APPLICANT: RAHAOUI, HAKIM
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TYPE: PRT
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ANKHLSILEDWNGKDPQYVN 94
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Pred. No. 0.0038;
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Pred. No. 0.23;
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Listing first 45 summaries
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=	hypothetical prote	exodeoxyribonuclea	probable membrane	hypothetical prote	glyceraldehyde-3-p	conserved hypothet	probable phosphodi	hypothetical prote							

## ALIGNMENTS

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A;Molecule type: DNA
A;Residues: 1-171,173-641,'N',643-1475 <SH2>
A;Experimental source: strain GS-5
C;Superfamily: cpl repeat homology
F;1096-1115/Domain: cpl repeat homology <CP1>
F;1224-1243/Domain: cpl repeat homology <CP2>
F;1289-1308/Domain: cpl repeat homology <CP3>
F;1354-1373/Domain: cpl repeat homology <CP3>
F;1354-1373/Domain: cpl repeat homology <CP5>
C;Accession: JT0345; C:31.3.
R;Ueda, S.; Shiroza, T.; Kuramitsu, H.K.
Gene 69, 101-109, 1988
A;Title: Sequence analysis of the gtfC gene from Streptococcus mutans GS-5.
A:Reference number: JT0345; MUID:89137980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Shiroza, T.; Ueda, S.; Kuramitsu, H.K.
J. Bacteriol. 169, 4263-4270, 1987
A;Title: Sequence analysis of the gtfB gene
A;Reference number: A33135; MUID:87308013
A;Accession: B33135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gtfB protein precursor - Streptococcus (;Speciles: Streptococcus mutans C;Date: 23-Oct-1900 #sequence_revision C;Accession: B33135; A33128 R;Shiroza, T; Ueda, S; Kuramitsu, H.K
                                                                                                                                          C;Species: Streptococcus mutans
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992
C;Accession: JT0345; C33135
                                                                                                                                                                                                                      dextransucrase (EC 2.4.1.5) precursor - Streptococcus mutans (strain GS-5) N; Alternate names: sucrose 6-glucosyltransferase
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                                                                                                                                                                                                                                                                            JT0345
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A; Accession: A33128
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A; Residues: 1-1475 <SHI>
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Best Local S
Matches 21
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Pred. No. 3.9e-10;
; Mismatches 0;
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F;1093-1112/bomain: cpl repeat hor F;1222-1241/Domain: cpl repeat hor F;1282-1306/Domain: cpl repeat hor F;1287-1306/Domain: cpl repeat hor F;1330-1351/Domain: cpl repeat hor F;1352-1371/Domain: cpl repeat hor F;1402-1420/Domain: cpl repeat hor F;1465-1484/Domain: cpl repeat hor F;1513-1532/Domain: cpl repeat hor F;165-1484/Domain: cpl repeat hor F;165-1484/Do
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A;Molecule type: DAA
A;Residues: 1-349 <SHI>
A;Cross-references: GB:M.
C;Genetics:
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J. Bacteriol. 169, 4263-4270, 1987
A;Title: Sequence analysis of the gtfB gene from Streptococcus mutans.
A;Reference number: A33135; MUID:87308013
A;Accession: C33135
                                                             RESULT
A41483
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C;Species: Streptococcus sobrinus
C;Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 15-Oct-1999
C;Accession: A38175
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A; Residues: 1-1375 <UED>
A; Experimental source: GS-5
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C;Function:
glucosyltransferase (EC 2.4.1.-)
C; Species: Streptococcus sobrinus
                                                                                                                                                                                          В
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Best Local S
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   Streptococcus sobrinus
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989-996, 1991
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No. 2.2e-08;
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Pred. No. 9.1e-09;
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                                                                                                                                                                                                                                                                                                              Mismatches
                                precursor
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A; Status: preliminary
A; Molecule type: DMA
A; Residues: 1-1431 <HON>
A; Residues: 1-1431 <HON>
A; Cross references: GB:M29296
C; Superfamily: Cpl repeat homology
C; Keywords: glycosyltransferase; hexosyltransfer.
F; 181-201/Domain: Cpl repeat homology <CPl>
F; 1192-1146/Domain: Cpl repeat homology <CP2>
F; 1192-1211/Domain: Cpl repeat homology <CP3>
F; 1257-1276/Domain: Cpl repeat homology <CP4>
F; 1277-1297/Domain: Cpl repeat homology <CP5>
F; 1321-1340/Domain: Cpl repeat homology <CP5>
F; 1341-1361/Domain: Cpl repeat homology <CP5>
F; 1341-1361/Domain: Cpl repeat homology <CP5>
F; 1341-1361/Domain: Cpl repeat homology <CP5>
F; 1385-1404/Domain: Cpl repeat homology <CP5>
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C;Superfamily: cpl repeat homology
C;Keywords: glycosyltransferase; h
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J. Gen. Microbiol. 136, 2099-2105, 1990
A;Title: Nucleotide sequence of the Streptococcus
A;Reference number: A45866; MUID:91100958
A;Accession: A45866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dextransucrase (EC 2.4.1.5) precursor - Streptococcus mutans C;Species: Streptococcus mutans C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999 C;Accession: A45866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Infect. Immun. 58, 2452-2458, 1990
A; Title: Analysis of the Streptococcus downei gtfS
A; Reference number: A41483; MUID: 90316665
                 C;Accession: T31098
R;Monchois, V.; Remaud-Simeon, M.; Monsan, FEMS Microbiol. Lett. 159, 307-315, 1998
A;Title: Cloning and sequencing of a gene ca;Reference number: Z20981; MUID:98164374
A;Accession: T31098
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A45866
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C;Accession: A41483
                                                                                                                                                             probable dextransucrase (EC 2.4.1.5), extracellular - Leuconostoc mesenteroides
C;Species: Leuconostoc mesenteroides
C;Date: 22-Oct_1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
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A; Residues: 1-1365 <GIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GB: M30943; NID: g153652; PIDN: AAA26898.1;
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Best Local Similarity
Matches 15; Conser
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Pred. No. 0.00087;
1; Mismatches 5;
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No.
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539 HLSILEAWSHNDAYYNED

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A; Molecule type: DNA
A; Residues: 1-1508 <MON>
A; Cross-references: EMBL: AF030129; NID: g2766611; PID: g2766612; PIDN: AAB95453.1
A; Experimental source: strain NRRL B-1299
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:L35495; NID:g662378; PID:g662379; PIDN:AAC41412.1
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C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999
C;Accession: T30857
             20
                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, February 1998 A;Description: Streptococcus salivarius V1477 gtfN. A;Reference number: 220854
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A; Residues: 1-1449 < JAF>
                                                                                                                                                                                                                                      A; Reference number: A; Accession: T30552
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                                                                                                                                                                  A;Cross-references: EMBL:AF049609; NID:g2935545; PID:g2935546; PIDN:AAC05156.1
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Species: Streptococcus salivarius
Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change
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                                                                                                                                                                                                                                                                                                                       Accession: T30552
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Best Local
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Best Local
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HLSILEAWSDNDTPYLHD
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13; Conserv
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72.2%;
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72.2%;
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                                               Score 66; DB Pred. No. 0.06 0; Mismatches
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Pred. No. 0.0041;
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Pred. No. 0.
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glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Leishmania mexicana (Species: Leishmania mexicana C;Species: Leishmania mexicana C;Species: Leishmania mexicana C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 11-Jun-1999 C;Accession: B48445; S25142
R;Hannaert, V.; Blaauw, M.; Kohl, L.; Allert, S.; Opperdoes, F.R.; Michels, P.A.M. Mol. Biochem. Parasitol. 55, 115-126, 1992
A;Title: Molecular analysis of the cytosolic and glycosomal glyceraldehyde-3-phosphat A;Reference number: A484445; MUID:93063042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Giffard, P.M.; Simpson, C.L.; Milward, C.P.; Jacques, N.A. J. Gen. Microbiol. 137, 2577-2593, 1991
A;Title: Molecular characterization of a cluster of at least A;Reference number: A44811; MUID:92148377
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A44811
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C;Species: Streptococcus salivarius
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 15-Oct-1999
C;Accession: A44811; S22726; S28809
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Infect. Immun. 63, 609-621, 1995
A;Title: Streptococcus salivarius ATCC 25975
A;Title: Streptococcus salivarius ATCC 25975
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C;Date: 22-Oct-1999
A; Reference number: A; Accession: B48445
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A; Residues: 1-1518 <GIF>
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A; Residues: 1-1577 <
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72.2%;
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Pred. No.
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submitted to the EMBL Data Library, February 1997
A;Bescription: Streptogramin B biosynthesis in Streptomyces pristinaesminn'.
A;Accession: T30289
A;Status: prolimins.
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A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-331 <HAN>
A:Cross references: EMBL:X65220; NID:g9552; PIDN:CAA46323.1;
C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C:Keywords: oxidoreductase
                                                                                                                                                                                                                                        pristinamycin I synthase 3 - Streptomyces pristinaespiralis C;Species: Streptomyces pristinaespiralis C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 01-Dec-2000 C;Accession: T30289 R;de Crecy-Lagard, V.A.; Saurin, W.; Thibaut, D.; Gil, P.; Naudin, L.; Croux
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Experimental source: ATCC 25975

R;Giffard, P.M.; Simpson, C.L.; Milward, C.P.; Jacques, N.A.

J. Gen. Microbiol. 137, 2577-2593, 1991

A;Title: Molecular characterization of a cluster of at least two glucosyltransferase A;Reference number: A44811; MUID:92148377

A;Accession: S28810
A; Gene: snbDE C; Superfamily: acyl carrier protein homology; acetate -- CoA ligase homology
                                                 A;Cross-references: EMBL:Y11548; NID:e1025755; PID:e307539; PIDN:CAA72312.1 C;Genetics:
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C;Keywords: glycosyltransferase; hexosyltrans
F;1456-1475/Domain: cpl repeat homology <CPR>
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A; Residues: 1-4848 <DEC>
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A; Residues: 1-51 <GIF>
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A; Residues: 1-1599 < JAC>
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C;Accession: S22737; S28810; B44811; S22727
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52.68;
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C;Species: Zea mays (maize)
C;Date: 23-Apr-1999 #sequence_revision 23-Ap
C;Accession: T03983
R;Cu1, X; Wise, R.P.; Schnable, P.S.
Science 272, 1334-1336, 1996
A;Title: The rf2 nuclear restorer gene of ma
A;Reference number: Z15177; MUID:96243131
A;Accession: T03983
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A; Note: rf2 C; Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase F; 107-370/Domain: aldehyde dehydrogenase homology <ALD>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T03983
rf2 nuclear restorer protein - maize
N;Alternate names: aldehyde dehydrogenase homolog
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A; Introns: 232/3;
A; Note: F18022.160
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8; Conservative
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ce: strain B73
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa//FCTUS_COMB.pep:*
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    DВ
               3 US-09-007-999-2

4 US-09-210-361-4

4 US-09-210-361-6

4 US-09-208-172-2

4 US-09-208-172-2

2 US-08-751-189-3

2 US-08-751-189-3

2 US-08-849-212-4

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2 US-08-849-212-4

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1 US-08-977-816-1

1 US-08-977-816-1

1 US-08-977-99-15

1 US-08-977-99-15

1 US-08-551-687-2

2 US-08-551-687-2

2 US-08-551-687-3

1 US-08-551-687-3
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4.898 Million cell updates/sec
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APPLICANT: Nichols, Scott E.

APPLICANT: Nichols, Scott E.

TITLE OF INVENTION: Substitutes for Modified Starches and
TITLE OF INVENTION: Latexes in Paper Manufacture
FILE REFERENCE: 0357CR
CURRENT APPLICATION NUMBER: US/09/210,361
CURRENT APPLICATION NUMBER: US/09/210,361
CURRENT FILING DATE: 1998-01-16
EARLIER APPLICATION NUMBER: 09/007,999
EARLIER APPLICATION NUMBER: 08/478,704
EARLIER FILING DATE: 1998-01-0
EARLIER APPLICATION NUMBER: 09/009,620
EARLIER APPLICATION NUMBER: 08/408,243
EARLIER FILING DATE: 1998-01-20
EARLIER APPLICATION NUMBER: 08/485,243
EARLIER FILING DATE: 1995-06-07
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US-09-007-999-2
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Best Local S
Matches 19
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	36.5	36.5	36.5	36.5	36.5	37	37	37	37	37	37	37	37	37	37	37	37	37
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ALIGNMENTS	US-08-722-258-1	US-08-225-224-1	US-08-463-480-1	US-08-461-234-1	US-08-405-615-1	PCT-US95-15646-2	US-08-668-650B-14	US-08-668-650B-2	US-08-566-096A-2	US-08-349-025-2	US-09-235-839-4	US-09-235-839-2	US-09-003-199-23	US-08-838-399-4	US-08-838-399-2	US-08-630-118A-4	US-08-630-118A-2	PCT-US95-15646-6
	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	μ,	Sequence 1, Appli	2, 1	Sequence 14, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 23, Appl	Sequence 4, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 6, Appli

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CURRENT APPLICATION NUMBER: US/09/007,999
CURRENT FILING DATE: 1998-01-16
EARLIER APPLICATION NUMBER: 08/478,704
EARLIER FILING DATE: 1995-06-07
NUMBER OF SEO ID NOS: 2
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1475
TYPE: PAT
ORGANISM: Streptococcus mutans
US-09-007-999-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 2, Application US/09007999
; Patent No. 6087559
; GENERAL INFORMATION:
; APPLICANT: Nichols, Scott E.
; TITLE OF INVENTION: Substitutes for Modified Starch
; TITLE OF INVENTION: Latexes in Paper Manufacture
; FILE REFERENCE: 0356D
                                                                                           l Similarity
19; Conserv
Application US/09210361
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Pred. No. 9e-09;
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Gaps

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APPLICANT: NICHOLS, Scott E.
APPLICANT: NICHOLS, Scott E.
TITLE OF INVENTION: Latexes in Paper Manufacture
FILE REFERENCE: 0357CR
CURRENT APPLICATION NUMBER: US/09/210,361
CURRENT FILING DATE: 1998-12-11
EARLIER APPLICATION NUMBER: 09/007,999
EARLIER FILING DATE: 1998-01-16
EARLIER FILING DATE: 1998-01-16
EARLIER FILING DATE: 1995-06-07
EARLIER FILING DATE: 1995-06-07
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 09/009,620
EARLIER APPLICATION NUMBER: 08/485,243
EARLIER APPLICATION NUMBER: 09/008,172
EARLIER APPLICATION NUMBER: 09/008,172
EARLIER FILING DATE: 1995-06-07
EARLIER FILING DATE: 1995-06-07
EARLIER FILING DATE: 1995-06-07
EARLIER FILING DATE: 1998-01-16
EARLIER RPPLICATION NUMBER: 08/482,711
EARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 6
EARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 6
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US-09-008-172-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT ; ORGANISM: Streptococcus mutans US-09-210-361-2
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                                                                                                                     Sequence 2, Application US/09008172 Patent No. 6127602 GENERAL INFORMATION:
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Best Local Similarity
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LENGTH: 1475
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                                   APPLICANT: Nichols, Scott E.
TITLE OF INVENTION: Substitutes for Modified Starch and
TITLE OF INVENTION: Latexes in Paper Manufacture
FILE REFERENCE: 0358D
CURRENT APPLICATION NUMBER: US/09/008,172
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EQ ID NO 4
LENGTH: 1375
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nes 18; Conserv
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b; Pred. No. 4.4
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Pred. No.
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; ORGANISM: streptococcus mutans US-09-210-361-6
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                                                                                                                                                                                      RESULT .
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                                                                                                          ; Patent No. 5981838
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: 08/478,704
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 09/009,620
EARLIER APPLICATION NUMBER: 08/485,243
EARLIER APPLICATION NUMBER: 08/485,243
EARLIER APPLICATION NUMBER: 09/008,172
EARLIER APPLICATION NUMBER: 09/008,172
EARLIER APPLICATION NUMBER: 08/482,711
EARLIER APPLICATION NUMBER: 08/482,711
EARLIER APPLICATION NUMBER: 08/482,711
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Best Local Similarity
Matches 13; Conserv
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EARLIER APPLICATION NUMBER: 08/482,711
EARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version :
SEQ ID NO 2
LENGTH: 1430
LENGTH: 1430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09210361
Patent No. 6284479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 6
                                                                                                                                           Sequence 2,
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Substitutes for Modified Starches TITLE OF INVENTION: Latexes in Paper Manufacture FILE REFERENCE: 0.357CR CURRENT APPLICATION NUMBER: US/09/210,361 CURRENT FILING DATE: 1998-12-11 EARLIER APPLICATION NUMBER: 09/007,999 EARLIER FILING DATE: 1998-01-16
             APPLICANT: Simpson, C
APPLICANT: Giffard, F
APPLICANT: Jacques, N
TITLE OF INVENTION: G
TITLE OF INVENTION: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 14
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Nichols,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
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576 NYIFIRAHDSEVQTVIA 592
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76.5%;
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76.5%;
                                Nicholas Anthony
Genetic Manipulation of Plants to
                                                                     Christine Lynn
Philip Morrison
Increase Stored Carbohydrates
2
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Pred. No.
                                                                                                                                                                                                                                                                                                                                 Score 65; I
Pred. No. 0.
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0.0026;
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CORRESPONDENCE ADDRESS:

ADDRESSEE: Griffith Hack & CO STREET: Level 8, 168 Walker St CITY: No. 5981838th Sydney STATE: New South Wales

168 Walker Street

COUNTRY:

Australia

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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08751189 Patent No. 5919656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: AU PM7643
FILING DATE: 24-AUG-1994
TELECOMMUNICATION INFORMATION:
TELEPHONE: 61 2 9957 5944
TELEPAX: 61 2 957 6288
TELEX: 26547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1577 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                 ATTORNEY/AGENT INFORMATION: NAME: Oleski, Nancy A.
                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               661 NYIFVRAHDSEVQAVLA 677
                                                                                                                                                                                                                                                  ADDRESSEE: Amgen, Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
NAME: Oleski, Nancy A. REGISTRATION NUMBER: 3
                                                 CLASSIFICATION:
                                                                 APPLICATION NUMBER: FILING DATE: 15-NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/793,824
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                                                                                                                                                                                                                                    California
                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                         Harrington, Lea A.
                                                                                                                                                                                                                                                                                                                                                                       Robinson,
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SYSTEM: PC-DOS/MS-DOS
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                                                               15-NOV-1996
                                                                                                                                                                                                                                                                                                                                                    , Murray O.
No. 5919656el Genes Encoding Telomerase Protein
                                                                                   US/08/751,189
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RESULT

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                                                                                                                                              ; MOLECULE TYPE: US-09-060-836-3
                                                                                                                                                                                                            CLASSIFLETION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/751,189
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-433
INFORMATION 50% SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2627 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09060836 Patent No. 5981707
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Best Local Similarity 47.1%;
Matches 8; Conservative
                                                                                Query Match
Best Local
                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Harringto
APPLICANT: Robinson,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 2627 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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205 MPSYSLSLGEEEEVEDL 221
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STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 91320-1789
                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: unl
                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: un
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                      1 VPSYSFIRAHDSEVQDL 17
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                                                               Similarity 47.1
8; Conservative
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Robinson, Murray C
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                                                                                44.28;
47.18;
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Pred. No.
                                                                                Score 42;
Pred. No.
                                                                 Mismatches
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85;
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US-09-184-445-3

Sequence 3, Application US/09184445 Patent No. 6174703

GENERAL INFORMATION:

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; MOLECULE TYPE: protein US-09-184-445-3
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US-08-849-212-4
                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08849212 Patent No. 5827698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: KIKUCHI,
APPLICANT: SUZUKI,
APPLICANT: KOJIMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 15-NOV-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Harrington, Lea A.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 6174703el Genes Encoding Telomerase Protein
TITLE OF INVENTION: 1
                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                         205 MPSYSLSLGEEEEVEDL 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Oleski, Ancy A.
REGISTRATION NUMBER: 34,68
REFERENCE/DOCKET NUMBER: F
                                                                                                      STREET: 1755 SOU
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                      COUNTRY:
                                                                                                                                          ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VPSYSFIRAHDSEVQDL 17
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California
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                                                                                                                      1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
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1840 De Havilland Drive
                                                                       USA
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                                                                                                                                                                                                              NOVEL LYSINE DECARBOXYLASE GENE AND METHOD OF PRODUCING L-LYSINE
                                                                                                                                                                                                                                                  HIROYUKI
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47.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                   APPLICATE: 21-AF: -
FILING DATE: 21-AF: JP
APPLICATION NUMBER: JP
----- DATE: 05-MAR-19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Yamano, Shiqeyuki
TITLE OF INVENTION: DNA SEQUENCES USEFUL FOR
TITLE OF INVENTION: SYNTHESIS OF CAROTENOIDS
                                                  FILING DATE: 19-APR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS: LENGTH: 713 amino acids
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APPLICATION NUMBER:
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                                                               FILING DATE: 05-MAK-1>>>
APPLICATION NUMBER: US 07/519,011
FILING DATE: 19-APR-1990
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                                                                                                                                                                                                                    APPLICATION NUMBER: J
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: UPPER NUMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: OBLON, NORMAN F REGISTRATION NUMBER:
NAME: Schwadron, Ja
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 LPLYAFINTHSTMDVSVQDM 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VPSYSFIRAH---DSEVQDL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New York
: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Application US/07783705A 5429939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 West 61 Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misawa, No. 54299:
Kobayashi, Kazuo
Nakamura, Katsumi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Diskette, 3.50 inch, 720Kb storage IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Linear
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09-JUN-1997
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45.0%;
                          Janet
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In Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18
                                                                                                                                                                                         JP 2-53225
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TELEFAX: 212-246-5959 INFORMATION FOR SEQ ID NO:

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TELEPHONE:

212-708-1935

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                                                         QY
                                                                                              Query Match
Best Local Similarity
Thes 9; Conserva
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Best Local Similarity 44.4%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (202)293-786
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Gubinsky, Louis
REGISTRATION NUMBER: 24,835
REFERENCE/DOCKET NUMBER: Q4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8-578-709-11
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LENGTH: 431 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 11
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: PH
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
168 SYSFLLRAGYLTLYGIEALPRTHESQAQDRV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 28-DEC CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/JP95/00838 FILING DATE: 27-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: UZIP: 20037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 PFYSHVRALQNLAQELVA 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: SUGHRUE, natur., STREET: 2100 Pennsylvania Avenue,
                                                                3 SYSFI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 PSYSFIRAHDSEVODLIA 19
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                                                                                                                                                                                                                                                                                                                                                           amino acid
GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                  237 amino acids
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                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUGHRUE, MION, ZINN, MACPEAK & SEAS
00 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMBER: US/08/578,709
28-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MBER: JP 114316/1994
28-APR-1994
                              PROSTACYCLIN SYNTHASE DERIVED FROM HUMAN
                                                                                                                                                              40.5%;
29.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11:
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                                                                                                                                                              Score 38.5;
Pred. No. 20;
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                                                                                                                             Mismatches
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                                                                                                                                                                                             DB 2;
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                                                                                                                                                                                         Length 237;
                                                                                                                             Indels
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US-08-977-816-1
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US-09-231-529-1
                                                                                                                                                                RESULT 14
                                                                                                                   Sequence 1, Application US/08977816 Patent No. 6194186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Applic Patent No. 6096308
                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                   GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Corley, Neil C.
                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linea
IMMEDIATE SOURCE:
LIBRARY: KIDNNC
CLONE: 353694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Incyte Pharmaceuticals,
NUMBER OF SEQUENCES:
                TITLE OF INVENTION:
                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                          111 VPSLEKVLEFKAHEGEIEDL 130
                                                                                                                                                                                                                                                                   Local Similarity
nes 8; Conserv
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CITY: Palo Alto
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STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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Corley, Neil C.
Chah, Purvi
Chah, Purvi
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Hillman, Jennifer L.
Randman, Olga
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                                                                                                                                                                                                                                                                                                Score 38.5;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.

STREET: 3174 POI CITY: Palo Alto

COUNTRY:

USA

CA

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В
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Best Local Similarity 40.0%;
Matches 8; Conservative
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08-578-709-15
Sequence 15, Application US/08578709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FASCLERO FOR WINDOWS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977
FILING DATE: Filed Herewith
CLASSIFICATION: 435
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TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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IMMEDIATE SOURCE:
KIDNNOT25
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J
PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                              APPLICANT: TANABE, Tadashi
TITLE OF INVENTION: PROSTAN
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 VPSLEKVLEFKAHEGEIEDL 130
                                APPLICATION NUMBER: US/0: FILING DATE: 28-DEC-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                       STREET: 2100 Penr
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
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CLONE: 353694
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                                                                                                                                                                                                            USA
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FastSEQ for Windows Version 2.0
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Pred. No. 32;
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Search completed: March 27, 2002, 13:59:27 Job time: 580 sec
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Best Local Similarity
Whiches 9; Conserva
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TELEPHONE: (202)293-7060
TELEPAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 114316/1994
FILING DATE: 28-APR-1994
                                                                                 168 SYSFLLRAGYLTLYGIEALPRTHESQAQDRV 198
                                                                                                                                                                                                                                                                                                                                                                                           NAME: Gubinsky, Louis
REGISTRATION NUMBER: 24,
REFERENCE/DOCKET NUMBER:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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GTFC_STRMU
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P13470; P05427;
01-NOV-1988 (Rel. 09, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GLUCOSYLTRANSFERASE-SI PRECURSOR (EC 2.4.1.5) (GTF
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EMBL; M22054; AAA88592.1; -.
EMBL; M17361; AAA88899.1; -.
PIR; JT0345; JT0345.
PIR; C33135; C33135.
InterPro; IPR002479; CW_binding.
                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                               Shiroza T., Ueda S., Kuramitsu H.K.;
"Sequence analysis of the gtfB gene from Streptococcus mutans.";
J. Bacteriol. 169:4263-4270(1987)
-i- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT
TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE
OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                          Ueda S., Shiroza T., Kuramitsu H.K.; "Sequence analysis of the gtfC gene Gene 69:101-109(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus mutans.
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=87308013; PubMed=3040685;
Shiroza T., Ueda S., Kuramitsu H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=89137980; PubMed=2976010;
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                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                  AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL) (N) =

D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL) (N+1).

SUBCELLULAR LOCATION: SECRETED.

DISEASE: DENTAL CARIES.
                                                                                                                                                                        FORMS OF GLUCANS.
SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES
BINDING PROTEIN FROM S.MUTANS.
                                                                                                                                                                                                               MISCELLANEOUS: GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES BOTH WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH
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SCK_HUMAN
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Streptococcus mutans.";

FEMS Microbiol. Lett. 161:331-336(1998).

FEMS Microbiol. Lett. 161:331-336(1998).

FINCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAU OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

-!- CATALYIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL) (N) =

D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL) (N+1).
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DOMAIN
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P08987; 069381; 069384; 069387; 069390; 069396;
01-NOV-1988 (Rel. 09, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GLUCOSYLTRANSFERASE-I PRECURSOR (EC 2.4.1.5) (GTF-I) (DEXTRANSUCRASE)
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REPEAT
                                                                                                                                                                                                                                                                                                               Fujiwara T., Terao Y.
Kimura S., Hamada S.;
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-MT4239, MT4245, MT4251, MT
MEDLINE-98231643; PubMed-9570124;
                                                                                                                                                                                                                                                                                                                                                                                                      Shiroza T., Ueda S., Kuramitsu H.K.; "Sequence analysis of the gtfB gene "Secteriol. 169:4263-4270(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus mutans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes;
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| Local Similarity
| Ches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUCROSE
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                                                  DISEASE: DENTAL CARIES.

MISCELLANEOUS: GTF-I SYNTHESIZES WATER-INSOLUBLE (1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S: WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI FORMS OF GLUCANS.

SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES AND SOMI BINDING PROTEIN FROM S.MUTANS.
       SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; PF01473; 
; PF02324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VPSYSFIRAHDSEVQDLI 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6-GLUCOSYLTRANSFERASE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CW_binding_1; 7
Glyco_hydro_70;
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AA; 1
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CATALYTIC (AAPROXIMATE).
GLUCAN-SIDDING (APPROXIMATE).
2.4 A, 1 C AND 1 AC REPEATS.
A REPEAT.
A REPEAT.
C REPEAT.
C REPEAT.
C REPEAT.
A REPEAT (INCOMPLETE).
A REPEAT (INCOMPLETE).
A REPEAT (INCOMPLETE).
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; Pred. No. 2.7;
0; Mismatches
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2.7e-07;
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                                                                     SOME
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S SYNTHESIZES BO
                                                                  TO A GLUCAN-
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         collaboration
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EMBL; M17361; AAA88588.1; --
EMBL; D88654; BAA26105.1; --
EMBL; D88654; BAA26109.1; --
EMBL; D88657; BAA26109.1; --
EMBL; D896659; BAA26113.1; --
EMBL; D89667; BAA26113.1; --
EMBL; D89977; BAA26113.1; --
PIR; B33135; B33135.
CONFLICT
SEQUENCE
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InterPro; IPR003318; Glyco_hydro_70.
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PF02324; Glyco_hydro_70;
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                                   H -> Y (IN STRAINS MT4245
G -> S (IN STRAINS MT4245
Y -> H (IN STRAINS MT4239,
AND MT8148).
H -> Y (IN STRAINS MT4245 A
G -> S (IN STRAINS MT4245 A
Y -> H (IN STRAIN MT4245 A
Y -> H (IN STRAIN MT4467).
R -> A (IN REF. 1)
                                                                                                                                                          MT8148)
A -> T
S -> N
H -> P
H -> P
H -> R
 WW. H
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NT -> SI
MT8148)
VDG -> /
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GLUCAN-BINDING (APPROXIMATE).
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           ADQDVRVAASTAPSTDGK (IN REF. 1).
H -> L (IN REF. 1)
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 3479B62B07694D98 CRC64;
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W (IN STRAIN MT4239).
Y (IN STRAIN MT4251).
K (IN STRAIN MT8148).
C (IN STRAIN MT8148).
P (IN STRAIN MT8148).
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P (IN STRAIN MT8148).
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Y (IN STRAIN MT8148).
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U (IN STRAIN MT8148).
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T (IN STRAINS MT4239).
1, MT4467 AND MT8148).
V (IN STRAIN MT4239).
P (IN STRAIN MT4251).
I (IN STRAIN MT4239).
F (IN STRAIN MT4239).
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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                    FGKPVE
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AND MT4251).
MT4245, MT42
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Matches
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GTF1_STRDO
                                                                                                                                                      InterPro; IPR003318; Glyco_hydro_70 Pfam; PF01473; CW_binding_1; 19. Pfam; PF02324; Glyco_hydro_70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Bacteriol. 169:4271-4278(1987).

-: FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAY OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIAN AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.
-:- CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N) D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N) -- SUBCELLULAR LOCATION: SECRETED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GLUCOSYLTRANSFERASE-I PRECURSOR (EC 2.4.1.5)
 REPEAT
REPEAT
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                                                                              DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                           <del>;</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus downei (Streptococcus sobrinus). Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                            EMBL; M17391; AAC63063.1;
                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                   SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sobrinus MFe28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ferretti J.J., Gilpin M.L., Russell R.R.B.; "Nucleotide sequence of a glucosyltransferase sobrinus MF2PA".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=87308014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-MFE28
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                                                                                                                                                                                                                                                                                                                                       FORMS OF GLUCANS.
SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES
BINDING PROTEIN FROM S.MUTANS.
                                                                                                                                                                                                                                                                                                                                                                                   DISEASE: DENTAL CARIES.
MISCELLANEOUS: GTF-I SYNTHESIZES WATER-INSOLUBLE (
1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S:
WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI
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Pred. No.
                                                                            CATALYTIC (APPROXIMATE).
GLUCAN-BINDING (APPROXIMATE)
1.25 A, 2 B, AND 5 AC REPEAT
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                                                                                                                   POTENTIAL.
GLUCOSYLTRANSFERASE-I
REPEAT.
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                                                                   REPEAT
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SYNTHESIZES
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P27470;
01-AUG-1992
01-AUG-1992
15-DEC-1998
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SEQUENCE
 CHAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GLUCOSYLTRANSFERASE-I PRECURSOR (EC 2.4.1.5)
                                    Transferase;
SIGNAL
                                                                                                              EMBL; D90213; BAA1424
PIR; A38175; A38175.
HSSP; P00695; 2HEE.
                                                                                                                                                                                           modified
                                                                                                                                                                                                      use
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synthetase).";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRDO
                                                            Pfam; PF01473; CW_binding_1; 16.
Pfam; PF02324; Glyco_hydro_70; 1.
                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                             entities requires
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Abo H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91123227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus downei (Streptococcus sobrinus).
                                                                                  InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
                                                                                                                                                                                                                                                                                                                                                                                                                                     -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Peptide sequences for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SUCROSE 6-GLUCOSYLTRANSFERASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    554 VPSYSFARAHDSEVQDLI 571
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriol. - FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VPSYSFIRAHDSEVQDLI
                                                                                                                                                                                                                                                                                                       MISCELLANEOUS: GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES B
                                                                                                                                                                                                                                                                                                                                                       AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS, CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N) D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).
SUBCELLULAR LOCATION: SECRETED.
                                                                                                                                                                                                                 European Bioinformatics Institute.
                                                                                                                                                                                                                                                                   SIMILATITY: TO OTHER GLUCOSYLTRANSFERASES BINDING PROTEIN FROM S.MUTANS.
                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE
                                                                                                                                                                                                                                                                                                                                              DISEASE: DENTAL CARIES
                                                                                                                                                                                                                                                                                            FORMS OF GLUCANS.
                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
17; Conserv
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                                                                                                                                                                                       non-profit institutions as long and this statement is not removed
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1519
1582
1597
Glycosyltransferase; Signa
1 38 POTENTIAL
39 1592 GLUCOSYLTR
39 1044 CATALYTIC
39 1592 GLUCAN-BIN
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                                                                                                                                       BAA14241.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sobrinus
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                                                                                                                                                                             a license agreement (See
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sucrose splitting and glucan binding glucosyltransferase (water-insoluble
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MW; B9E86
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Pred. No.
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AC REPEAT.
           GLUCOSYLTRANSFERASE-I.
CATALYTIC (APPROXIMATE)
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                                                Signal;
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                                                Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fukui K.,
                                                                                                                                                                           http://www.isb-sib.ch/announce/
                                                                                                                                                                                       Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GTF-I) (DEXTRANSUCRASE)
                                                                                                                                                                                                                                                                                AND
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                                                                                                                                                                                                                                                                               SOME
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                                                  Dental
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glucan
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Matches 16
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                                    PIR; A41483; A41483.
InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 10.
Pfam; PF02324; Glyco_hydro_70; 1.
                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
GLUCOSYLTRANSFERASE-S PRECURSOR (EC 2.4.1.5) (GTF-S) (DEXTRANSUCRASE)
(SUCROSE 6-GLUCOSYLTRANSFERASE).
                                                                                                                                                   use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                     This
                                                                                                                                                                                                                                                                                                                                                                                               Gilmore K.S., Russell R.R., Ferretti J.J.;
"Analysis of the Streptococcus downei gtfs gene, which specifies glucosyltransferase that synthesizes soluble glucans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTFS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
REPEAT
                Transferase; Glycosyltransferase; Signal; Repeat; Dental caries. SIGNAL 1 36 OR 37 (POTENTIAL).
                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                          the European Bioinformatics Institute. There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90316665; PubMed=2142479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus downei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P29336;
01-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTFS_STRDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VPSYSFIRAHDSEVQDLI 18
                                                                                                                                                                                                                                                                                                            ect. Immun. 58:2452-2458(1990).

FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N) = D.FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N)
                                                                                                                                                                                                                                       1,6-GLUCOSE
                                                                                                                                                                                                                                                             DISEASE: DENTAL CARIES MISCELLANEOUS: GTF-S SI
                                                                                                                                                                                                                                                                                       ENZYME REGULATION: GLUCAN SYNTHESIS PRIMER GLUCAN UNLIKE GTF-I.
                                                                                                                                                                                                                            BINDING PROTEIN FROM
                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a centre the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VPSYSFARAHDSEVQDII 565
                                                                                                   M30943; AAA26898.1; -.
                                                                                                                                                                                                                                                   6-GLUCOSE)
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1142
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1451
1563
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; Bacillus/Clostridium group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 98;
                                                                                                                                                                                                                           GLUCOSYLTRANSFERASES S.MUTANS.
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Pred.
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      GLUCOSYLTRANSFERASE-S
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  (See http://www.isb-sib.ch/announce/
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Best Local
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01-FEB-1996 (Rel. 33, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GLUCOSYLTRANSFERASE-S PRECURSOR (EC 2.4.1.5
                                                                                                                                                                                                                                                                                                                                                                                     "Nucleotide sequence of the Streptococcus the jucosyltransferase-S enzyme.":
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DOMAIN
                                              between the Swiss Institute of Bioinf
the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                       Fujiwara T., Terao Y., Hoshino T., Kawabato
Kimura S., Hamada S.;
"Molecular analyses of glucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTFD_STRMU
                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                    Streptococcus mutans."; FEMS Microbiol. Lett. 161:331-336(1998)
                                                                                                                                                                                                                                                                                                                                STRAIN=MT4239, MT4245, MT4251, MT4467, AND MEDLINE=98231643; PubMed=9570124;
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                               WEDLINE=91100958; PubMed=2148600;
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-GS-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VPSYSFIRAHDSEVQDLIA
                                                                                                                              MISCELLANEOUS: GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,3-LINKED GLUCOSE AND SOME 1,6-LINKAGES), GTF-S SYNTHESIZES MATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH
                                                                                                                                                                                                       TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUTO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUTHER ABILITY TO ADHERE TO SMOOTH SUFFACES AND MEDIATE THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N) -
                                                                                              SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES AND SOME TO A GLUCAN-BINDING PROTEIN FROM S.MUTANS.
                                                                                                                                                                       DISEASE: DENTAL CARIES.
                                                                                                                                                                                D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).
SUBCELLULAR LOCATION: SECRETED.
                                                                                                                      FORMS OF GLUCANS
                                                                      SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VPNYVFIRAHDSEVQTRIA 555
                                                                                                                                                                                                                                                                                                                                                                                 cosyltransferase-S enzyme.";
Microbiol. 136:2099-2105(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Firmicutes;
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78.9%;
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                                                        yright. It is produced through of Bioinformatics and the EN
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Pred. No.
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4.5 X TANDEM REPEATS.
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                                                                                                                                                                                                                                                                                                                     Kawabata
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2.4.1.5)
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EMBL; EMBL;

, M29296; AAA26895.1; ...
, D88653; BAA26103.1; ...
, D88656; BAA26107.1; ...
, D88659; BAA2611.1; ...
, D88662; BAA26115.1; ...
, D89979; BAA26121.1; ...

EMBL;

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8
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Best Local S
Matches 13
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InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 11.
Pfam; PF02324; Glyco_hydro_70; 1.
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                                    68.4%;
76.5%;
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A -> S (IN STRAIN MT4239).
TDQGSEA -> ADKGNDS (IN STRAIN MT4251).
TDQGS -> ADKGN (IN STRAINS MT4239 AND MT4245).
D -> Y (IN STRAIN MT4251).
E -> K (IN STRAINS MT4245 AND MT4251).
                           Score 65; DB Pred. No. 0.00 2; Mismatches
                                                                                                                                       LG -> IR (IN STRAIN
G -> R (IN STRAIN MT
G -> R (IN STRAIN MT
Q -> H (IN STRAINS MT
Q -> H (IN STRAINS MT
Q -> H (IN STRAIN MT
Q -> L (IN STRAIN MT
Y -> C (IN STRAIN MT
Y -> C (IN STRAIN MT
Q -> P (IN STRAIN MT
Q -> P (IN STRAIN MT
N -> D (IN STRAIN MT
N -> G (IN STRAIN MT
N -> G (IN STRAIN MT
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S -> A (IN
AND MT8148)
A -> V (IN
V -> L (IN
D -> N (IN
D -> D (IN
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D -> N ()
MT4251).
Q -> H ()
D -> N ()
E -> K ()
V -> F ()
                                                                                                   R -> G (IN STRAINS MT4239, MT4251, MT4467 AND MT8148). R -> K (IN STRAIN MT4467).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
GLUCOSYLTRANSFERASE-S.
3 X 63 AA APPROXIMATE
                                                                                 RYYDKNSGNMVYNKVVTLANGRRIGIDRWGIARYY VYR (IN REF. 1).
                                                                                                                               AND MT8148;
                                                                                                                                                                                                                                                                                                                     MT4467).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * * * * *
                                                                                                                                      -> R (IN STRAIN MT4239).
-> H (IN STRAINS MT4239, MT4245,
4251, MT4467 AND MT8148).
-> N (IN STRAIN MT4239).
-> C (IN STRAIN MT4251 AND MT4467).
-> L (IN STRAIN MT4467).
-> P (IN STRAIN MT4245).
-> T (IN STRAIN MT4245).
-> G (IN STRAIN MT4245).
-> G (IN STRAIN MT4239, MT4245, MT425).
                                                                         5C6541F0DCB0DF00 CRC64
                                                                                                                                                                                                                                   > IR (IN STRAIN MT4251).
R (IN STRAIN MT4245).
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                                                                                                                                                                                                                                                                                                                              H (IN STRAIN MT4245).
N (IN STRAINS MT4239)
K (IN STRAIN MT4239).
F (IN STRAIN MT4239).
L (IN STRAINS MT4239).
                                                                                                                                                                                                                                                                                                                                                                                     (IN STRAINS MT4239,
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                                    DB 1;
0.007;
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N STRAIN MT4239).
N STRAIN MT8148).
N STRAINS MT4239,
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N STRAINS MT4239 i
N STRAINS MT4251 i
N STRAINS MT4239 i
N STRAINS MT4239,
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STRAINS MT4239 AND
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                             Indels
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AND MT8148).

AND MT4245).

MT4245 AND
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                            Gaps
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RESULT 7
COMA_BACS 7
COMA_BACS 7
COMA_BACS 7
COMA_BACS 7
101-JAN
DT 01-JAN
D
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Query Match
Best Local Similarity 52...
Ches 9; Conservative
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01-JAN-1990 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
3 COMPETENCE PROTEIN A.
COMA OR COMAA OR COMA1.
Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium granderia; Firmicutes; Bacillus/Bacillus.
                                                                                                                                                                                                                                                                                                                                                                               InterPro: IPR000792; HTH_Luxr.
InterPro: IPR001789; Response_reg
Pfam; PF00196; GerE; 1.
Pfam; PF00072; response_reg; 1.
SMART; SM00421; HTH_LUXR; 1.
SMART; SM00448; REC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMA_BACSU
P14204;
01-JAN-1990
                                                                                                                                                                                   MOD_RES
DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                    PROSITE; PS00622; HTH_LUXR_FAMILY; 1.
Sensory transduction; Phosphorylation; Transcription regulation;
DNA-binding; Activator; Complete proteome.
DNAIN 1 101 RECEIVER DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M22856; AAA22320.1; -. EMBL; Z93932; CAB07904.1; -. EMBL; Z99120; CAB15156.1; -. PIR; A33591; RGBSCA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produ between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oudega B., Koningsteijn G., Van Zoest A.;
Submitted (APR-1997) to the EMBLYODBJ databases.
SUBTILIS, FOR THE EXPRESSION OF LATE-EXPRESSING COMPETENCE
SUBTILIS, FOR THE EXPRESSION OF LATE-EXPRESSING COMPETENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence and transcription mapping of Bacill genes come and come, one of which is related regulatory determinants.";
J. Bacteriol. 171:5362-5375(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SubtiList; BG10381; comA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=90008771; PubMed=2507523;
Weinrauch Y., Guillen N., Dubnau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: PHOSPHORYLATED BY COMP.
SIMILARITY: TO OTHER BACTERIAL REGULATORY PROTEINS INVOLVED IN SIGNAL TRANSDUCTION.
SIMILARITY: BELONGS TO THE LUXR/UHPA FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENES, AND FOR THE EXPRESSION OF THE GROWTH STAGE-REGULATED MOLECULE SURPACTIN. MAY PLAY A REGULATORY ROLE DURING THE DEVELOPMENT OF COMPETENCE, AND AN ANALOGOUS ROLE AS UVC-CRF2 (TRANSDUCING ENVIRONMENTAL INFORMATION TO THE DNA REPAIR SYSTEM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGULATORS
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171
                                                                                                                                                                                      AA;
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                                                                                                                                                                                      WW.
                                                                                                                                                                                   PHOSPHORYLATION (BY SIMILARITY).
H-T-H MOTIF (BY SIMILARITY).
; 52D01A9740759072 CRC64;
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45.3%; 52.9%;

Score 43; DB Pred. No. 4.4;

Length 214; Indels

Mismatches

0;

Gaps

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PSYSFIRAHDSEVQDLI

18

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RESULT
RNB_ECC
RNBAC P.
DT 0.
DT 0.
DT 2.
DT 2.
DT E.
CGN RR
GN RR
GOC BB
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STANDARD,
P30850; P78280;
01-UU-1993 (Rel. 26, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                 DNA Res. 3:363-377(1996).

-I- FUNCTION: INVOLVED IN MRNA DEGRADATION. HYDROLYZES SINGLE-STRANDED POLYRIBONUCLEOTIDES PROCESSIVELY IN THE 3' TO 5' DIRECTION.

-I- CATALYTIC ACTIVITY: EXONUCLEOLYTIC CLEAVAGE IN THE 3' TO 5' DIRECTION TO YIELD 5'-PHOSPHOMONONUCLEOTIDES.

-I- SUBCELLULAR LOCATION: CYTOPLASMIC.

-I- SIMILARITY: BELONGS TO THE RIBONUCLEASE II (RNB) FAMILY.

-I- SIMILARITY: CONTAINS 1 'S1 MOTIF' DOMAIN.
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                  Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Ito Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Mashino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Sai Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Takeuchi S.) DNA Sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map."; DNA Res. 3:363-377(1996).
                                                                                            use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVISIONS.
Zilhao R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "DNA sequencing and expression of the coll ribonuclease II."; Mol. Microbiol. 8:43-51(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-93268098; PubMed-8497196;
Zilhao R., Camelo L., Arraiano C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97251357; PubMed-9097039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted
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                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Eleuropean Bioinformatics Institute. There are no rest
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complete genome sequence nce 277:1453-1474(1997).
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                       X67913; CAA48112.1; -. AE000226; AAC74368.1; D90767; BAA14848.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli K-12.";
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                                                                                                            http://www.isb-sib.ch/announce/
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                                                                                                                              Usage
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Best Local
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InterPro: IPR001900; Ribonuclease_II.
InterPro: IPR003029; S1.
InterPro: IPR003029; S1.
Pfam: PF00773; RNB; 1.
SMART: SM00357; CSP; 1.
SMART: SM00357; CSP; 1.
SMART: SM00316; S1; 1.
PROSITE: PS01175; RIBONUCLEASE_II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                               influenzae Rg.;
Science 269:496-512(1995).
-!- FUNCTION: INVOLVED IN MRNA DEGRADATION.
-!- FUNCTION: INVOLVED PROCESSIVELY IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fledds C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase;
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
EXORIBONICLEASE II (EC 3.1.13.1) (RIBONICLEASE II) (RNASE II).
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EcoGene; EG11620; rr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=RD / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Whole-genome random sequencing influenzae Rd.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
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                                                                                                                                                                                                                              CATALYTIC ACTIVITY: EXONUCLEOLYTIC CLEAVAGE IN THE 3' TO DIRECTION TO YIELD 5'-PHOSPHOMONOUCLEOTIDES.
SUMCELJULAR LOCATION: CYTOPLASMIC (BY SIMILARITY)
SIMILARITY: BELONGS TO THE RIBONUCLEASE II (RNB) FAMILY.
SIMILARITY: CONTAINS 1 'S1 MOTIF' DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ø
                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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$32940; $32940
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8; Conser
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513
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399 C
513 A
72490 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gamma subdivision; Pasteurellaceae;
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Pred. No.
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22;
                                                                                                                                                                                                                                                                                                                                                                                       HYDROLYZES SINGLE-STRANDED 3' TO 5' DIRECTION
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(See http://www.isb-sib.ch/announce,

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Best Local S
Matches
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15-JUL-1998 (Rel.
15-JUL-1998 (Rel.
15-JUL-1998 (Rel.
                                                                                                                                                                                                                                       the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. U
                                                                                                                                                                                                                                                                                                           Wood V., Rajandream M.A., Barrell B.G., Pohl T.;
Submitted (JUN-1997) to the EMBL/GenBank/DBBJ databases.
-I- FUNCTION: COULD PLAY A PART IN MECHANISMS OF TRANSCRIPTIONAL
REGULATION SIMILAR TO THAT PLAYED BY YEAST HIR1 AND HIR2 TOGE
-!- SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).
-!- SIMILARITY: BELONGS TO THE HIR1 FAMILY OF WD-REPEAT PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
InterPro;
InterPro;
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TIGR;
          REPEAT
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15-JUL-1998 (Rel. 36,
15-JUL-1998 (Rel. 36,
HISTONE TRANSCRIPTION
                                                                                                                                               PRINTS; PR00320; GPROTEINBRPT.
SMART; SM00320; WD40; 6.
                                                                                                                                                                       InterPro; IPR001680; WD40. Pfam; PF00400; WD40; 6.
                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS01175; RIBONUCLEASE_II; 1.
Hydrolase; Exonuclease; Nuclease; RNA-binding; CSEQUENCE 659 AA; 75782 MW; FDADA9097A7D3B66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART;
                                                                                                  Hypothetical
                                                                                                                 PROSITE;
                                                                                                                        PROSITE; PS00678;
PROSITE; PS50082;
                                                                                                                                                                                            EMBL; Z97204; CAB10089.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=97
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                                                                               REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2
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T; SM00357; CSP; 1.
T; SM00316; S1; 1.
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HI1733; -.
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                                                                                                                 PS50294;
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IPR001900; Ribonucleas
16
72
132
174
268
320
623
664
                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                               WD_REPEATS_REGION; 1.
                                                                                                                         WD_REPEATS_1; 1. WD_REPEATS_2; 4.
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171
171
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                                                                                                                                                                                                                             tatement is not removed. Usage by and for commercial license agreement (See http://www.isb-sib.ch/announce/
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Last annotation updat
REGULATOR 1 HOMOLOG.
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                                                                                                   Transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomycetaceae;
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Pred.
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87654321
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                                                                                                   regulation; Repeat; WD repeat;
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22;
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                                                                                                                                                                                                                                                                                       collaboration
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RESULT
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Best Local
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                                                                                      SEQUENCE SCHRAMM S., Duncan.
Schramm S., Duncan.
Davis K., Federspiel N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DCLZ_ECOLI STANDARE P52095; P78299; 01-0CT-1996 (Rel. 34, CO1-NOV-1997 (Rel. 35, IO)-NOV-1997 (Rel. 40, IO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Characterization of a second Escherichia coli.";
MEDLINE=98389317; PubMed=9723924; Pichoff S., Alibaud L., Guedant A "An Escherichia coli gene (yaeO)
                                                                                                                                                                                         STRAIN-K12 / W3110;
Takemoto K., Mori H., Murayama N., Kataoka K., Yano M., Itoh T.,
Yamamoto Y., Inokuchi H., Miki T., Hatada E., Fukuda R., Ichihara S.,
Mizuno T., Yakino K., Nakata A., Yura T., Sampei G., Mizobuchi K.;
                                                                                                                                                                                                                                                                  "The complexe genome sequence of Escherichia coli K-12."; Science 27: 1453-1474(1997).
                                                                                                                                                                                                                                                                                          Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Snay Y.,
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                                                                                                                                                                                                                                             SEQUENCE FROM M.A.
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STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                            Genes
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97480927; PubMed-9339543;
Yamamoto Y., Miwa Y., Miyoshi K., Furuya
"The Escherichia coli ldcC gene encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE STRAIN=K12 / W3110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97369816; F
Kikuchi Y., Kojima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli
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                                                SEQUENCE
                                                                                   Davis R.W
                                                                                                                                                                                                                                                                                                                                            MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia
                                                                                                                                                        "Systematic sequencing of the Escherichia coli genome: analysis 4.0 - 6.0 min (189,987 - 281,416bp) region."; submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteriol. 179:4486-4492(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=9226257;
                                                                                                                       3
                                                                                                                                                                                                                                                                                                                                                                                           utive enzyme.";
72:167-172(1997).
                                                FROM
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Last annotation
CONSTITUTIVE (EV
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                                                                                                          Allen E., Araujo R.,
., Hyman R., Kalman S
             Guedant A.,
                                                                                             Hyman
                                                N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gamma
                                                                        EMBL/GenBank/DDBJ databases
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                                                                                             Namath A.,
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1 lysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 subdivision;
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suppresses
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(EC 4.1.1.18) (LDC)
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            Castanie
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decarboxylase
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32;
                                                                                               Oefner P.,
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                                                                                                         Aparicio A., ., Komp C., K
 temperature-sensitive
           м.-Р.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   415-456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterobacteriaceae;
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           Bouche J.
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RESULT 12
MIZD_BACSU
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AC P26935
AC P26935
DT 01-AUG
DT 01-AUG
DT WYO-IN
GN IDH OR
OS Bactill
OC Bacter
OC Bactill
OX NCBI_T
RN [1]
RP SEQUEN
RA FUJILA
RT "Bacil
RT Sequen
RL Gene 1
RN [2]
RP SEQUEN
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Best Local S
Matches 9
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EMBL; D49445; BAA08426.1; --
EMBL; BA000128; AAC73297.1; --
EMBL; D83536; BAA77861.1; --
EMBL; U70214; AAB08615.1; --
EMBL; U70214; AAB08615.1; --
EMBL; Z0870; CAA90749.1; --
ECOGene; EG13219; ldcC.
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CONFLICT
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SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P26935;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18).
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                                                                      MEDLINE=92104493; PubMed=1761221;
Fujita Y., Shindo K., Miwa Y., Yoshida K.;
"Bacillus subtilis inositol dehydrogenase-encoding
sequence and expression in Escherichia coli.";
Gene 108:121-125(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mutations in essential genes by modulating Rho-dependent transcription termination.";
Mol. Microbiol 29:859-869(1998).

-I- FUNCTION: LDC IS CONSTITUTIVELY BUT WEAKLY EXPRESSED CONDITIONS. OPTIMUM ACTIVITY IS ACHIEVED BETWEEN PH 6-1- CATALYTIC ACTIVITY: L-LYSINE - CADAVERINE + CO(2).

-I- COFACTOR: PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                 Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium group;
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                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                        Bacillus/Staphylococcus
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SIMILARITY: BELONGS TO FAMILY 1 OF
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01276; OKR_DC_1; 1.
PS00703; OKR_DC_1; 1.
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713
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S -> T (IN REF. 2).

N -> F (IN REF. 2).

T -> S (IN REF. 2).

AA -> R (IN REF. 2).

M -> I (IN REF. 2).

L -> I (IN REF. 2).
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Pred. No. 29;
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Best Local
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EMBL; D14399; BAA03296.1; -.
EMBL; 299124; CAB16006.1; -.
PIR; JH0511; JH0511.
SubtiList; BG10669; idh.
InterPro; IPR000683; GFO_IDH_MOCA.
Pfam; PF01408; GFO_IDH_MOCA; 1.
                                                                                                                                                                                                                                                                                                                                                 ADEN_ADEG8
Q9QM72;
                             "The DNA sequence of fowl adenovirus 8.";

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

1. FUNCTION: THIOL PROTEASE CLEAVING SPECIFIC GLY-ALA PEPTIDES IN A UNDBER OF VIRAL PRECURSOR PROTEINS (TERMINAL, IIIA, VI, VII, VIII, IIA AND MU) WHICH ARE REQUIRED FOR VIRION MATURATION. ALSO CLEAVES HOST CELLS CYTOSKELETAL KERATINS X7 AND K18.

1. CATALYTIC ACTIVITY: CLEAVES PROTEINS OF THE ADENOVIRUS AND ITS HOST CELL AT TWO CONSENSUS SITES: -YAA-XAA-GLY-GLY-|-XAA-AND -YAA-XAA-GLY-XAA-|-GLY-(IN WHICH YAA IS MET, ILE OR LEU, AND XAA IS ANY XAA-GLY-XAA-|-GLY-(IN WHICH YAA IS MET, ILE OR LEU, AND XAA IS ANY
                                                                                                                                                                                                                                           20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
ADENAIN (EC 3.4.22.39) (ENNOPROTEASE) (LATE L3 23 KDA PROTEIN).
Avian adenovirus type 8 (strain ATCC A-2A) (Fowl adenovirus 8).
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Aviadenoviru
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Microbiology 140:2289-2298(1994).
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MEDLINE=95039891; PubMed=7952181;
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CATALYTIC ACTIVITY: MYO-INOSITOL +
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PATHWAY: FIRST STEP OF MYO-INOSITOL CATABOLISM SUBUNIT: MONOMER.
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SIMILARITY: BELONGS TO
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01-MAY-1991 (Rel. 18,
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SEQUENCE
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Nakamura K., Harashima K.;
"Elucidation of the Erwinia uredovora
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                    PROSITE; PS00375; UDPGT; 1.
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- FUNCTION: CATALYZES THE GLYCOSYLATION REACTION
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PATHWAY: CAROTENOID BIOSYNTHESIS.
SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                            European Bioinformatics Institute.
                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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                                                                                                                                            s requires a license agreement (S an email to license@isb-sib.ch).
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STRAIN-ATCC 14830;
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MEDLINE-92305068; PubMed-1610906;
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SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
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Pfam; PF01473; CW_binding_1; 7.
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"Molecular analyses of glucosyltransferase
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MEDLINE=98231643; PubMed=9570124;
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Pfam; PF01473; CW_binding_1; 10.
Pfam; PF02324; Glyco_hydro_70; 1.
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Kimura S., Hamada S.;
"Molecular analyses of glucosyltransferase
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069391;
       Streptococcus mutans.";
FEMS Microbiol. Lett. 161:331-336(1998)
EMBL, D89978; BAASG120.1;
InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1: 9.
Pfam; PF02324; Glyco_hydro_70; 1.
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GLUCOSYLTRANSFERASE-SI.
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                                                                          "Molecular analyses of
                                                                                            MEDLINE=98231643; PubMed=9570124; Fujiwara T., Terao Y., Hoshino T.,
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NCBI_TaxID=1309;
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"Molecular analyses of glucosyltransferase
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Fujiwara T., Tera
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EMBL; D88661; BAA26114.1; -.
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Q55263;
       MEDLINE-94146405; PubMed-8312602;
Sato S., Inoue M., Handa N., Alzawa Y., Isobe Y., Katayama T.,
"DNA sequence of the glucosyltransferase gene of serotype d
Streptococcus sobrinus.";
DNA seq. 4:19-27(1993).
-1- CATALYTIC ACTIVITY: SUCROSE + ((1,6)-ALPHA-D-GLUCOSYL)(N)
ENGL: D13858; BAA02976.1;
EMBL; D13858; BAA02976.1;
                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 17, Last annotation update)
GLUCOSYLTRANSFERASE-I PRECURSOR (EC 2.4.1.5) (DEXTRANSUCRASE) (SUCROSE
                                                                                                                                                                                                                                                                                                                                                                                             Ann. Kagoshima Univ. Dental School 16:23-29(1996).
EMBL: D63570; BAA09792.1; -
InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 15.
Pfam; PF01473; CW_binding_1; 15.
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GLUCOSYLTRANSFERASE GTF-I.
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NCBI_TaxID=1310;
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GLUCOSYLTRANSFERASE (EC
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                NCBI_TaxID=1245;
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Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ250172; CAB76565.1; -
InterPro; IPR0032479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PP01473; CW_binding_1; 14.
Pfam; PP01473; CW_binding_1; 14.
Pfam; PP01473; CW_binding_1; 14.
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Pfam; PF02324; Glyco_hydro_70; 1.
Signal; Transferase; Glycosyltransferase.
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CHAIN 39 1590 GLUCOSYLTRANSFERASE-I.
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SEQUENCE FROM N.A
                                                          Bacillus/Clostridium
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                                                                                                                  Last sequence update)
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.1.5) (DEXTRANSUCRASE) (
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1; Mismatches
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01-MAR-2001 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
DEXTRANSUCRASE DSRB742.
                                                                                                                                                          01-MAY-1999
01-MAY-1999
01-JUN-2001
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FEMS Microbiol. Lett. 0:0-0(1998).
-1- CATALYTIC ACTIVITY: SUCROSE + ((1,6)-ALPHA-D-GLUCOSYL)(N) =
FRUCTOSE + ((1,6)-ALPHA-D-GLUCOSYL)(N+1).
EMBL; AF030129; AAB95453.1;
-1.
InterPro; IPR003219; Glyco_hydro_70.
pfam; PF003318; Glyco_hydro_70.
pfam; PF01473; CW_binding_1: 14.
pfam; PF01473; CW_binding_1: 14.
pfam; PF01324; Glyco_hydro_70; 1.
Transferase; Glyco_hydro_70; 1.
Transferase; Glyco_syltransferase.
SEQUENCE 1508 AA; 168511 MW; E70CECB57A70D1F0 CRC64;
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InterPro; IPR003318; Glyco.hydro_70.
Pfam; PF01473; CW_binding_1; 14.
Pfam; PF02324; Glyco.hydro_70; 1.
SEQUENCE 1508 AA; 168542 MW; E2F
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Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
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                                                                      Bacteria;
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"Leuconostoc mensenteroides B-742CB, a dextransucrase gene.";
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                       NCBI_TaxID-1245;
                                                                 Leuconostoc mesenteroides
Bacteria; Firmicutes; Bac
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73.7%;
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73.7%;
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Pred. No. 7.26
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RESULT
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Q9LCJ7;
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Q48756;
01-NOV-1996
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STRAIN=NRRL B-512-F;
Bhatnagar R., Singh D.K.S.;
Bhotnagar R., Singh D.K.S.;
"Cloning and Molecular Characterization
"Cloning and mesenteroides NRRL B-512F.";
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Pfam; PFC
SEQUENCE
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SEQUENCE FROM N.A.
STRAIN-NRRL B1299,
MEDLINE-97136686; PubMed-8982063;
MOnchois V. Willemot R.M., Remand-Simeon M
Monchois V. Willemot R.M. a gene coding fo
"Cloning and sequencing of a gene coding fo
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InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 16.
Pfam; PF02324; Glyco_hydro_70; 1.
SEQUENCE 1527 AA; 169709 MW; 1DF
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Submitted (DEC-1996) to the EMBL/GenBank/DDBJ
EMBL; U81374; AAD10952.1; -
                                  DSRT
                                                                                                                                                                                                                                                                                                                    from Leuconostoc mesenteroides 6) and alpha (1-3) linkages."; Gene 182:23-32(1996).
EMBL: U38181; AAB40875.1;
           Leuconostoc mesentero Bacteria; Firmicutes;
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InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 11.
Pfam; PF02324; Glyco_hydro_70; 1.
SEQUENCE 1290 AA; 145590 MW; 355
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Racteria; Firmicutes;
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Pred. No. 7.3e
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RESULT 15
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SEQUENCE
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                                                                         GTF-S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "S.cricetus glucosyltransferase(gtfS and gtfT) genes."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases EMBL; AB026123; BAA77237.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid pam1.
Bacteria; Firmicutes;
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STRAIR-NRRL B-511F;
MEDLINE-20169623; PubMed-10705445;
Funane K., Mizuno K., Takahara H., Kobayashi M.;
Streptococcus criceti. Plasmid pAM1.
                                                                                                                        01-NOV-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 14.
Pfam; PF02324; Glyco_hydro_70; 1.
                                                                                                  01-JUN-2001
                                                                                                                                                                                                 Q9WXJ4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=HS-6;
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                                                                                                                                                                        Q9WXJ4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inoue M., Fukui K., Miyagi A.;
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nes 14; Conserv
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1 (TrEMBLrel.
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77.8%;
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77.88;
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17,
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Last sequence update)
Last annotation updat
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Last sequence update)
Last annotation update)
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Job time: 1674 sec
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Best Local :
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                                                                                                                                                                              Plasmid.
SEQUENCE
                                                                                                                                                                                                                                                    "S.Cricetus glucosyltransferase(gtfS and gtfT) genes.";
"S.Cricetus glucosyltransferase(gtfS and gtfT) genes.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AB026123; BAA77236.1; -.
HSSP; P06278; 1VJS.
                                                                                                                                                                                                  InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 10.
Pfam; PF02324; Glyco_hydro_70; 1.
                                                                                                                                                                                                                                                                                                                  STRAIN-HS-6;
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae; Streptococcus.
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1333;
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                                                              509
                                                           1 VPSYSFIRAHDSEVQDLIA 19
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09 VPNYVFIRAHDSEVQTRIA 52
                                                                                                              1 Similarity
15; Conserv
                                                                                                                                                                             1338 AA;
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           27,
                                                                                                                        76.8%;
78.9%;
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           2002,
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Pred. No. 0.001;
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                                                                                                                                      Length 1338;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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AAW87970
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GT subsequence. S
GTF antigenic pept
GTF antigenic pept
GTF antigenic pept
GILOSY, Irransferea
Alpha-D-glucosyltr
L. mesenteroides a
Toxin A immunogeni
C. difficile toxin
C. difficile toxin
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High molecular wei	AAR41724	14	1477	38.4	43	45
Haemophilus	AAB01849	21	1036	38.4	43	44
Human polypeptide	AAM41533	22	380	38.4	43	43
Human	AAM39747	22	349	38.4	43	42
Streptococcus	AAY71284	21	153	•	43	41
C glutamicum prote	AAG90590	22	196		43.5	40
Amino acid sequenc	AAY54411	21	181	•	44	39
Protein encoded by	AAY54410	21	121	•	44	3 8
Human secreted	AAG00949	21	94	•	44	37
Arabidopsis	AAG31198	21	630		45	36
Arabidopsis	AAG31199	21	563	40.2	45	ω 5
. Toxin A immunogeni	AAW87968	20	204	40.2	45	34
Acid alpha-amylase	AAR28304	13	1301	•	46	ω ω
Streptococcus	AAY81652	21	745	41.1	46	32
	AAR73912	16	684	41.1	46	31
S. pneumoniae	AAW92456	20	653	41.1	46	30
PspA fragment	AAR27150	13	653	41.1	46	29
A pneumococcal	AAW87879	20	648	41.1	46	28
Streptococcus	AAY41837	20	648	41.1	46	27
Streptococcus	AAW62274	19	648	41.1	46	26
Pneumococcal	AAW70336	19	648	41.1	46	25
Streptococcus	AAW61217	19	641	41.1	46	24
Streptococcus	AAY41838	20	619	41.1	46	23
Pneumococcal	AAR86911	17	619	41.1	46	22
Pneumococcal	AAR87598	17	619	41.1	46	21
Pneumococcal	AAR63437	15	619		46	20
Human polypeptide	AAM41179	22	794		47	19
Human	AAM39393	22	785		47	18
P. fal	AAB45695	22	337		49	17
Clostridium diffic	AAW68387	19	2710		49.5	16
C. difficile	AAR95016	17	2710	44.2	49.5	15
A recombinant	AAB30546	21	866	44.2		14
A recombinant	AAB30543	21	866	44.2	49.5	13
Toxin A	AAW87971	20	862	44.2	49.5	12

#### ALIGNMENTS

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AAR43696
                                                                                                                                                                                                                                               RESULT
                                                                                                                                                       GT; glucosyitransferase; vaccine; T-cell; B-cell; reaction;
immunoresponse; peptidyl core matrix; dental caries; diptheria;
tetanus; measles; polio.
                                                                               01-MAY-1992;
                                                                                                                                         Synthetic.
                                                                                                                                                                                   GT subsequence.
                                                                                                                                                                                                                                AAR43696 standard;
                                   WPI; 1993-368721/46
                                                 Smith DJ,
                                                                                            30-APR-1993;
                                                                                                                          W09322341-A
                                                                                                                                                                                                  20-MAY-1994 (first entry)
                                                                                                                                                                                                                  AAR43696;
                                                               (FORS-) FORSYTH DENTAL INFIRMARY FOR CHILDREN
                                                                                                           11-NOV-1993
                                                                                                                                                                                                                                              ш
                                                 Taubman MA;
                                                                               92US-0877295
                                                                                            93WO-US04094
                                                                                                                                                                                                                               peptide;
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Claim 3; Page 23; 38pp; English

Synthetic glucosyl-transferase peptide(s) - provoke T- and B-cell reactions in mammals, and are effective against dental caries

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RESULT
AAW34159
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Best Local
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glucosyltransferase in a mammal. The immune response results in reduction of the colonisation or accumulation of mutans streptococcal strains in the mammal. Compositions containing AAW34156 specifically interfere with the glucan-binding activity of the streptococcal glucosyltransferase. The peptides can also be used in vaccines for
                                                                                                                                                                                                           AAW34156-W34160 represent immunogenic fragments of the Streptomyces mutans glucosyltransferase (GTF) enzyme. AAW34157 and AAW34158 are from the catalytic domain of GTF, while AAW34160 is from the GTF surface domain. AAW34156 and AAW34159 are from the glucan-binding domain of GTF. These sequences can all be used in the immunogenic composition of the invention. The composition of the invention can alternatively comprise one or more of these sequences linked to a lysine core matrix (see AAW34161-W34165). A composition comprising one of these sequences can be administered to a mammal to refere a formal control of these sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glucosyltransferase; GTF; enzyme; immunogen; catalytic domain; vaccine; surface domain; glucan-binding domain; mutans streptococcal strain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenic compositions containing streptococcal glucosyl:transferase peptide(s) - used for provoking immune respon to streptococcal glucosyl:transferase for preventing dental caries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-558089/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FORS-) FORSYTH DENTAL INFIRMARY FOR CHILDREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-APR-1993;
01-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5686075-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTF antigenic peptide #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                core matrix. They are useful in producing T-cell responses to the GT enzyme causing a reduction of colonisation or accumulation of mutans steptococcal strains in mammals. The vaccines can be us
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequences (AAR43694-98) are subsequences from GT, they prove T- and B-cell responses in mammals. The can be used to produce vaccine comprising 2 of these sequences attached to a peptidyl
                                                                                                                                                           administered to a mammal to raise an immune response, in a method interfering with the enzymatic activity of streptococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1992;
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glucan-binding activity; dental caries prevention.
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                                                             compositions, are used to induce an antibody response to cariogenic bacteria, collectively called "mutans streptococci" (i.e. any of Streptococcus mutans, S. rattus, S. cricetus or S. sobrinus), especially to prevent colonisation, to reduce numbers of bacteria or to reduce incidence of caries, in humans or other animals. The composition can therefore be used for the treatment or prevention of caries (particularly dental caries). Abs raised against (A) can be used: (a) to detect SG, and (b) for passive immunisation, e.g. applied directly to the surface of teeth. SG is a poorly immunogenic type 2 T-cell independent antigen but when coupled to (I) it produces a conjugate which induces significant immunity to both components, resulting in immunological memory and
                                                                                                                                                                                                                                                                                                                                                 This sequence represents a glucosyltransferase (GTF) immunogenic epitope and can be used in the immunogenic composition of the invention. The immunogenic composition of the invention of the invention of the invention of the invention. The immunogenic composition (A) comprises at least one streptococcal glucan (SG) and at least one component (I) covalently coupled, (in)directly, to SG. (A) elicits antibodies (Ab) to both SG and (I). (A) and related the invention of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunogenic compositions for control of dental caries, based on Streptococcus mutans components, particularly for vaccination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTF; antigenic epitope; glucosyltransferase; immunogenic epitop immunogenic composition; streptococcal glucan; antibody respons cariogenic bacteria; mutans streptococci; colonisation; caries;
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polylysine core. AAW34157 and AAW34158 are from the GTF, while AAW34160 is from the GTF surface domain. are from the glucan-binding domain of GTF. These sec immunogenic fragments shown in AAW34156-W34160 can a
                                                                                                                    Immunogenic compositions containing streptococcal
glucosyl:transferase peptide(s) - used for provoking
to streptococcal glucosyl:transferase for preventing
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17; Conserv
                                                                                               Column
                                                                                                                                                                                                     Taubman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mutans
                                                                                                                                                                                                                                                        93US-0057162.
92US-0877295.
                                                                                                                                                                                                                                                                                               92US-0877295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label=
/note= '
                            represent the Streptomyces mutans glycosyltransferase unogenic fragments shown in AAW34156-W34160 linked to a AAW34157 and AAW34158 are from the catalytic domain of 160 is from the GTF surface domain. AAW34156 and AAW34159
                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                             -; 11pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.78;
77.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #4 linked
                                                                                                                                                                                                                                                                                                                                                                         "the alpha amino acid group of Lys(24) forms a peptide linkage with the carboxyl amino group o Lys(23); the omega amino group of Lys(24) forms a peptide bond with a second Lys residue analogous to Lys(23)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "attached to the dendritic polylysine core via
the alpha-amino group of Lys(23); a second co
of the antigenic 22-mer is linked to Lys(23)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Lys(23)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTF antigenic peptide #4 (see AAW34159)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       omega amino group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lys(23) is linked the peptide through the second copy of the
                                                                                              English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        omega amino group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 87; DB 20;
Pred. No. 2.2e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  o one copy of the antigenic alpha-amino group, and to peptide (not shown) via the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ω,.
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dental caries
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1 TGARTINGQLLYFRANGVQVKG

22 2;

Query Match Best Local

Matches

l Similarity 17; Conserv

Conservative

77.78; 77.38;

Score Pred.

87;

DB 1, 4.5e-06;

Length 1592;

Mismatches

Indels

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AAR32925
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Best Local
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                                   glucosyltransferase-I (and mutants). The DNA was obtd. by treating S. sobrinus 6715 with mutanolysin, extracting the chromosomal DNA, partially digesting with Sau3AI and fractionating on agarose gel. The 3-5 kbp fragment was ligated into pUC18 and E. coli yM109 transformed with it. A GT-1 expressing clone was isolated and sequenced. The clone may be used in the development of a drug for
                                                                                                                                                                                                                                                              (FUKU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        results in reduction of the colonisation or accumulation of mutans streptococcal strains in the mammal. Compositions containing AAW34156 specifically interfere with the glucan-binding activity of the
                                                                                                                                                                                DNA sequence glucosyl:transferase-I - comprises Streptococcus sobrinus DNA sequence with at least one nucleotide added or
                                                                                                                                                                                                                                                                                                                                                                                 JP05023188-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glucosyltransferease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                streptococcal glucosyltransferase. The peptides can also be used in vaccines for preventing dental caries in mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunogenic composition of the invention. A composition comprising one these sequences can be administered to a mammal to raise an immune response, in a method for interfering with the enzymatic activity of streptococcal glucosyltransferase in a mammal. The immune response
Sequence
                         dental caries.
                                                                                                                  The DNA
                                                                                                                                           Claim 13;
                                                                                                                                                                     deleted
                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                    WPI; 1993-079449/10.
                                                                                                                                                                                                                                                                                                     25-JUL-1991;
                                                                                                                                                                                                                                                                                                                              25-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                       02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                   GT-1;
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| 1 tgaqtikgqklyfkangqqvkg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TGARTINGQLLYFRANGVQVKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
17; Conserv
                                                                                                                                                                                                                                                              KATO :
                                                                                                               sequence from Streptococcus sobrinus strain
                                                                                                                                                                                                                        AAQ37760
 1592
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                                                                                                                                                                                                                                                                                                                                                                                                           sobrinus
                                                                                                                                          15;
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                                                                                                                                                                                                                                                                                                                               91JP-0186592
 AA;
                                                                                                                                       29pp; Japanese.
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77.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                   dental;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     caries
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2.5e-08;
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                                                                                                                  6715
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RESULT 7
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                                                                                                                            Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                    Streptococcus salivarius. The enzyme is primer-independent, and produces soluble glucan from sucrose. A gene encoding the enzyme may be cloned and expressed in Escherichia coli using a subclone of phage lambda-Cl3, e.g. plasmid pGSG501 or plasmid pGSG502. The DNA may also be expressed in a transgenic plant, to improve the level of stored carbohydrate in a pasture plant which normally contains low levels, or to prevent degradation of stored carbohydrate during plant senescence. Dextran may be isolated from the plant, for use as a food binder or pharmaceutical additive. Primer independence ensures that the enzyme will be functional in plants. The glucan is poorly degraded in plants but easily degraded by bacteria in the rumer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GIFF/)
                                                                   1469
                                                                                                                                                                                                                                                                                                                                                                                          The sequence represents an alpha-D-glucosyltransferase from Streptococcus salivarius. The enzyme is primer-independent, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sucrose; transgenic plant; cloning; Escherichia coli; phage lambda-C13; vector; plasmid pGSG501; plasmid pGSG502; gene transfer; crop improvement; storage carbohydrate; pasture; feedstuff; senescence; dextran; binder; food; pharmaceutical.
                                                                                                                                                                                                                               of grazing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plants contg. new bacterial DNA encoding glucosyl transferase activity - retain higher levels of stored carbohydrate(s) in a form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-151376/15.
N-PSDB; AAT13139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Giffard PM, Jacques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alpha-D-glucosyltransferase;
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                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 16-20; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   readily digestible by ruminants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-AUG-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alpha-D-glucosyltransferase
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                                                                 tglqnlnnkvyyfgsngaqvkg 1490
                                                                                             TGARTINGOLLYFRANGVOVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) GIFFARD P M.
) JACQUES N A.
) SIMPSON C L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                 livestock.
                                                                                                                                                                                                     1577
                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95WO-AU00527
                                                                                                                                                                                                     AA;
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                                                                                                                                        58.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NA,
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                                                                                                                          4.
                                                                                                                                         Score 66;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primer-independent; soluble glucan;
                                                                                                                            Mismatches
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                                                                                                                                         DB 17;
0.02;
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                                                                                                                                                       Length 1577;
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XXX DXX XXX
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                                                                                                                                  RESULT
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Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                               glucosyltransferase group) The recombinant, purified alternan sucrase gene is useful for the fermentative production of alternan (a carbohydrate) and/or fructose by secreting the enzyme into a saccharose-containing culture medium. Alternatively, the enzyme is contacted with a saccharose-containing solution. The alternan and/or fructose is then isolated from the medium. Cosmetic products or foodstuffs containing alternan can be produced. Recombinant production alternan sucrase is advantageous as it provides a cost effective means producing fructose for high fructose containing syrups, production of which previously has been achieved by costly production from maize starch. This sequence represents the Leuconostoc mesenteroides alternan
                                                                                                                                                                                                                                                                                                                       starch. This sequence represents the Leuconostoc mesenteroides alternan sucrase protein which is described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel nucleic acid molecule (I) encoding an alternan sucrase (E.C. 2.4\cdot1.140 - an enzyme, that belongs to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim la; Page 30-36; 64pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alternan sucrase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PLAN-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alternan sucrase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB10667;
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                       Toxin A immunogenic fragment p5/6.
                                                   29-APR-1999
                                                                             AAW87969;
                                                                                                       AAW87969
                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         syrup
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid
                                                                                                                                                                        261 glqtidgnlqyfnqqgvqikg
                                                                                                                                                                                                                             Local Similarity les 12; Conserv
                                                                                                                                                                                      2 GARTINGQLLYFRANGVQVKG 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLANTTEC BIOTECHNOLOGIE GMBH.
                                                                                                       standard;
                                                                                                                                                                                                                                                                                               2057 AA;
                                                                                                                                                                                                                             Conservative
                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoding
protein a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glucosyltransferase; fructose; cosmetic; foodstuff;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'n,
                                                                                                       peptide;
                                                                                                                                                                                                                                        58.0%;
57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g recombinant Leuconostoc mesenteroides and methods of alternan and fructose
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Pred. No. 0.
                                                                                                         A
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of of

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Toxin A; immunogenic fragment; vaccine; diagnosis; infection.

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RESULT
AAW87970
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Best Local
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                     (QUEE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents an immunogenic fragment of Clostridium difficile (CD) Toxin A, designated fragment p5/6. This sequence is encoded by nucleotides 7159-8118 of the Toxin A gene. The invention relates to fragments of toxin A of CD which are non-toxic and immunogenic. They can be used in the preparation of vaccines against to infection. The amino acid molecules and antibodies against them can be used in the preparation of an agent for the prophylaxis or treatment of a CD infection. They can also be used for detection and diagnosis of CD infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JAN-1998;
20-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clostridium difficile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 6; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated Clostridium difficile proteins - comprise fragments toxin A, used to develop agents for prophylaxis, treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Douce
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 Douce
                                                     07-JAN-1998;
20-JUN-1997;
                                                                                                          30-DEC-1998
                                                                                                                                                       Clostridium difficile
                                                                                                                                                                           Toxin A;
                                                                                                                                                                                                 Toxin A
                                                                                                                                                                                                                       29-APR-1999
                                                                                                                                                                                                                                            AAW87970
                                                                                                                                                                                                                                                                AAW87970 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                     19-JUN-1998;
                                                                                                                                                                                                                                                                                                                       74
                                                                                                                                                                                                                                                                                                                                           1 TGARTINGQLLYFRAN-GVQVKG 22
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                                                                                                                                                                                                                                                                                                                      tglrtidgkkyyfntntavavtg
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                     IMPERIAL COLLEGE SCI TECHNOLOGY & QUEEN MARY & WESTFIELD COLLEGE.
                                                                                                                                                                                                immunogenic
                                                                                                                                                                                                                                                                                                                                                                             Similarity
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s of C. difficile infect
                                                                                                                                                                          immunogenic fragment; vaccine; diagnosis; infection
Dougan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dougan G,
                                                                                                                                                                                                                                                                                                                                                                                                                        320 AA;
                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                      (first entry)
                                                     98GB-0000321.
97GB-0013146.
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97GB-0013146.
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                                                                                     98WO-GB01805
                                                                                                                                                                                                                                                                peptide;
                                                                                                                                                                                                fragment
                                                                                                                                                                                                                                                                                                                                                                             44.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ward
 Ward SJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infections
                                                                                                                                                                                                                                                                 457
                                                                                                                                                                                                                                                                                                                                                                 Score 49.5; I
Pred. No. 2;
2; Mismatches
                                                                                                                                                                                                                                                                                                                       96
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                                MED.
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Best Local
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16-MAR-1995;
14-APR-1995;
A recombinant protein (AAR95014) comprises amino acids 1870-2680 of Clostridium difficile VPI strain 10463 toxin A (see also AAR95016), a cytotoxin associated with diarrhoetic disease. It was obtd. by
                                                                                                                                                              Firca JR, Williams
                                                                         C. difficile type toxins,
partic. diarrhoea
                                                  Claim 53;
                                                                                   Fusion proteins comprising non-toxin protein and part of toxin useful to form anti-toxins against Clostridium botulinum type A, C. difficile type toxins, and to treat C. difficile intoxication,
                                                                                                                                                                                                                                                                                                                                         WO9612802-A1
                                                                                                                                                                                                                                                                                                                                                                                          diarrhoea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents an immunogenic fragment of Clostridium difficile (CD) Toxin A, designated fragment p5/7. This sequence is encoded by nucleotides 6748-8118 of the Toxin A gene. The invention relates to fragments of toxin A of CD which are non-toxic and immunogenic. They can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated Clostridium difficile proteins - cortoxin A, used to develop agents for prophylaxis, diagnosis of C. difficile infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                       WPI; 1996-230603/23
                                                                                                                                                                                                                                                                07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                02-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                Clostridium difficile VPI strain 10463 (ATCC 10463).
                                                                                                                                                                                                                                                                                                                                                                                                     Toxin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Fig 7; 82pp; English.
                                                                                                                                                                                                    (OPHI-) OPHIDIAN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 tglrtidgkkyyfntntavavtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used in the preparation of vaccines against CD infection. The amino an agent for the prophylaxis or treatment of a CD infection. They can so be used for detection and diagnosis of treatment of a CD infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10
                                                                                                                                                                                                                                                                                                                                                                                                                            difficile toxin A (aa1870-2680).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TGARTINGQLLYFRAN-GVQVKG 22
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                                                                                                                                                               JA;
                                                                                                                                                                                                                                                                                                                                                                                                    cytotoxin;
                                                  Page 310-312; 434pp; English
                                                                                                                                                                                                                                                                                                                                                                                      ytotoxin; enterotoxin; diagnosis; therapy.
                                                                                                                                                                           Kink JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                          95US-0480604.
94US-0329154.
95US-0405496.
95US-0422711.
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                                                                                                                                                                                                                                                                                         95WO-US13737
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52.2%;
                                                                                                                                                                          Padhye NV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
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Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                           Stafford
                                                                                                                                                                                                                                                                                                                                                                                                    fusion
                                                                                                                                                                                                                                                                                                                                                                                                   protein; antitoxin;
                                                                                                                                                                           g,
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Best Local S
Matches 12
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             Query Match
Best Local
                                                                               A protein (AAR95017) comprising amino acids 1873-2684 of Clostridium difficile VPI strain 10463 toxin A (see also AAR95016) was obtd. by PCR amplification of genomic DNA. The PCR product can be expressed in transformed E. coli host cells as a soluble fusion protein, with maltose binding protein or a polyhistidine affinity tag as fusion partner. The resulting soluble fusion proteins, which are substantially endotoxin-free, can be used in anti-clostridial antitoxin therapy for humans and animals.
                                                                                                                                                                                                                                                                                                                                                                          24-OCT-1994;
16-MAR-1995;
14-APR-1995;
                                                                                                                                                                                                                                         Fusion proteins comprising non-toxin protein and part of toxin useful to form anti-toxins against Clostridium botulinum type A, C. difficile type toxins, and to treat C. difficile intoxication,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium difficile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C. difficile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR amplification of genomic DNA, and was expressed as a soluble fusion protein, with maltose binding protein as fusion partner, in transformed E. coil host cells. The soluble fusion protein can be used to raise avian antibodies useful as antitoxins or diagnostics.
                                                           Sequence
                                                                                                                                                                                                        Claim 79; Page 354-356;
                                                                                                                                                                                                                                                                                           WPI; 1996-230603/23.
                                                                                                                                                                                                                                                                                                                  Williams
                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toxin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR95017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      587
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 1 Similarity
12; Conserv
                                                                                                                                                                                                                                 diarrhoea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytotoxin; e
n; diarrhoea;
                                                                                                                                                                                                                                                                                                                             Kink JA,
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                                                           812
  Conservative
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94US-0329154.
95US-0405496.
95US-0422711.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     95WO-US13737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A (aa1873-2684).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enterotoxin;
             44.2%;
52.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.28; 52.28;
                                                                                                                                                                                                                                                                                                                            Padhye NV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VPI strain 10463 (ATCC 10463).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis;
                                                                                                                                                                                                       434pp; English.
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Score 49.5; D
Pred. No. 6.4;
2; Mismatches
 2;
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Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fusion protein; antitoxin;
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                        17;
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                                                                                                RESULT
                                                                                                                                                                      Query Match
Best Local Similarity
Matches 12; Conserv
           A recombinant
                                                                                                                                                                                                                                             This sequence represents an immunogenic fragment of Clostridium difficile (CD) Toxin A, designated fragment p9/10. This sequence is encoded by nucleotides 530-8115 of the Toxin A gene. The invention relates to fragments of toxin A of CD which are non-toxic and immunogenic. They can be used in the preparation of vaccines against to infection. The amino acid molecules and antibodies against them can be used in the preparation of an agent for the prophylaxis or treatment of a CD infection. They can also be used for detection and diagnosis of CD infection.
                                                                                                                                                                                                                                                                                                                                                                 New isolated Clostridium difficile proteins - comprise fractoxin A, used to develop agents for prophylaxis, treatment diagnosis of C. difficile infections
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                                                     AAB30543;
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20-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Toxin A;
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                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunogenic fragment; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Dougan
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                                                                                                                                                                        Conservative
                                (first entry)
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           protein of toxin
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97GB-0013146
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                                                                         Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fragment
                                                                                                                                                                                 44.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Ward
                                                                                                                                                                                                                                                                                                                                                                                                                                  , LS
                                                                                                                                                                      score 49.5; D
pred. No. 6.9;
2; Mismatches
                                                                          866
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           A repeating
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                                                                                                                                                                                              DB
           units (rARU).
                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                                                                                                                       comprise fragments
                                                                                                                                                                                           Length
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                                                                                                                   RESULT 14
AAB30546
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Best Local
                                                                                                                                                                                                                       Matches
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01-MAR-2000;
20-MAR-2000;
                                                                                                                                                                                                                                                                                                                    The present sequence represents a Clostridium difficile recombinant protein comprising toxin A repeating units (rARU). The protein is used to prepare recombinant protein components. These recombinant protein components comprise at least one repeating unit of Clostridium difficile toxin A (rARU), one repeating unit of Clostridium difficile toxin B (rBRU), or both. The recombinant protein is used as a vaccines, and is useful for conferring a protective response in a mammalian host. It is also useful for producing antibodies for passive immune therapy against a strain of Clostridium difficile. The vaccines, formulated for use in humans and animals, is useful for treating Clostridium difficile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Toxin A passive
 Toxin A; repeating unit; rARU;
                        A recombinant protein of toxin A repeating units (rARU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenic composition for use as a vaccine against Clostridium difficile, comprises recombinant protein component consisting of at least one repeating unit of toxin A or toxin B or both, of Clostridium difficile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
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                                                     06-MAR-2001
                                                                                                     AAB30546 standard;
                                                                                                                                                                                                                                                                                     Sequence
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immune therapy;
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                                                                                                                                                                                                                                                                                     866 AA;
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                                                    (first entry)
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821..822
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                                                                                                     Protein;
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52.28;
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                                                                                                       866
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                                                                                                                                                                                                                                  Score 49.5; DI Pred. No. 6.9;
immunogenic composition; polysaccharide;
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Misc-difference 821..822
AAR95016;
                                                                                                                                                                                                                                                                                                                                                                                 nosocomial pathogenic microorganism. The immunogenic compositions are useful as vaccines for humans, particularly children and animals in affording protection against one or more microbial pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                             synthesized. The immunogenic compositions are useful for eliciting a protective immune response (T-cell dependent or T-cell independent, a cellular or humoral immune response) to a strain of pathogenic microorganism. The immunogenic composition also elicits a protective immune response against the polysaccharide produced by a strain of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     component, in which the recombinant protein is encoded by a gene from a strain of Clostridium difficile and the polysaccharide component is isolated from a strain of pathogenic microorganism or is chemically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein comprising toxin A repeating units (rARU). The protein is used to prepare immunogenic compositions of the invention. The immunogenic compositions comprise a recombinant protein and a polysaccharide
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01-MAR-2000;
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immune response.
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US DEPT HEALTH & HUMAN SERVICES
                                        standard;
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52.2%;
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difficile toxin

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                                                                                                                                                                                                                                             Clostridium difficile VPI strain 10463 toxin A (AAR95016), the product of the toxin A gene (AAR79248), is a potent cytotoxin that plays a direct role in damaging gastrointestinal tissues and is associated with diarrheetic disease. It can be obtd. by expression in transformed E. coli hosts of portions of DNA that together cover the entire toxin A gene. Toxin A, and portions of it (see also AAR95014-15 and AAR95017), pref. expressed as fusions to polyhistidine affinity tags or maltose binding protein, are used to raise avian antibodies useful as antitoxins or diagnostics, and in vaccine prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995;
24-OCT-1994;
16-MAR-1995;
14-APR-1995;
                                                                        1 TGARTINGQLLYFRAN-GVQVKG 22
|| || || :| : || || || || 2460 tg1rt1dgkkyyfntntavavtg 2482
                                                                                                                                                                                                                                                                                                                                                                                                                                        Fusion proteins comprising non-toxin protein and part of toxin useful to form anti-toxins against Clostridium botulinum type A, and C. difficile type toxins, and to treat C. difficile intoxication, partic. diarrhoea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9612802-A1
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                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 63; Page 290-302; 434pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-230603/23.
N-PSDB; AAT29248.
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Williams JA;
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                                                                                                                                                                                                                      2710 AA;
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94US-0329154.
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Pred. No. 29;
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

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15:105 Million cell updates/sec

Title:
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Sequence:
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Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched:
100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters:
100059

Maximum DB seq length: 0
Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SwissProt\_39:\*

## SUMMARIES

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## ALIGNMENTS

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between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).  EMBL; M17361; AAA88588.1; EMBL; D88651; BAA26101.1; EMBL; D88654; BAA26105.1;	1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE), GTF-SI SYNTHESIZES BOTH FORMS OF GLUCANS!- SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES AND SOME TO A GLUCAN- BINDING PROTEIN FROM S.MUTANS.	GLUCANS, THOUSEN DEPTH NEW THOUSE AND DEBRIS. HA-D-SLUCO	MEDLINE-87308013; PubMed=3040685; Shiroza T., Ueda S., Kuramitsu H.K.; "Sequence analysis of the 9tfB gene from Streptococcus mutans."; J. Bacteriol. 169:4263-4270(1987). [2] [2] [2] SEQUENCE FROM N.A. STRAIN-MT4239, MT4245, MT4251, MT4467, AND MT8148; MEDLINE-98231643; PubMed=9570124; Fujiwara T., Terao Y., Hoshino T., Kawabata S., Ooshima T., Sobue S., Kimura S., Hamada S.; "Molecular analyses of glucosyltransferase genes among strains of Streptococcus mutans.";	JLT 1 3_STRMU STANDARD; PRT; 1476 AA. GTFB_STRMU STANDARD; PRT; 1476 AA. P08987; 069381; 069384; 069387; 069396; 01-NOV-1988 (Rel. 09, Created) 15-JUI-1999 (Rel. 38, Last sequence update) 15-JUI-1999 (Rel. 38, Last sequence update) GLUCOSYLTRANSFERASE-I PRECURSOR (EC 2.4.1.5) (GTF-I) (DEXTRANSUCRASE) GSUCOSYLTRANSFERASE). GTFB. (SUCROSE 6-GLUCOSYLTRANSFERASE). Streptococcus mutans. Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcus. NCBI_TaxID=1309; [1] STERINGES_FGH N.A.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D88657; BAA26109.1;
EMBL; D88660; BAA26113.1;
EMBL; D89977; BAA26119.1;
PIR; B33135; B33135.
                                                                                                                        VARIANT
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         TGARTINGQLLYFRANGVQVKG
  TGARTINGQHLYFRANGVQVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                           PF01473; CW_binding_1; 1: PF02324; Glyco_hydro_70;
                                  Similarity
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AA; 165685
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CATALYTIC (APPROXIMATE).
GLUCAN-BINDING (APPROXIMATE).
A REPEAT.
5 X TANDEM REPEATS.
1.
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                                                           ADQDVRVAASTAPSTDGK -> (IN REF. 1).
H -> L (IN REF. 1).
MW; 3479B62B07694D98 (
                                                                                      AND MT8148)
H -> Y (IN S
G -> S (IN S
Y -> H (IN S
Y -> A (IN I
                                                                                                                     MT4251)
H -> Y
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NT -> :
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No. 7
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Y (IN STRAIN MT8148).
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MT4467 AND MT8148).
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N STRAIN MT4251).
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STRAIN MT8148)
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                                  DB 1;
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                                        Length 1476;
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AND MT4251).
MT4245, MT4
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                           Gaps
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Query Match
Best Local Similarity
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RESULT 2

GTF2_STRDO
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AC P27470
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P27470;
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
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01-AUG-1992 (Rel. 23, Last sequence
15-DEC-1998 (Rel. 37, Last annotatic
GLUCOSYLTRANSFERASE-I PRECURSOR (EC
(SUCROSE 6-GLUCOSYLTRANSFERASE).
                                                                                         REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D90213; BAA14241.1;
PIR; A38175; A38175.
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    SEQUENCE
                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                  InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 16.
Pfam; PF02324; Glyco_hydro_70; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kagawa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91123227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus downei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N)
D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).
SUBCELLULAR LOCATION: SECRETED.
DISEASE: DENTAL CARIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE OF THEIR ABILLTY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

CAPALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N) =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MISCELLANEOUS: GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (AL
1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES
WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES BINDING PROTEIN FROM S.MUTANS.
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pean Bioinformatics Institute. There are no rest
non-profit institutions as long as its content
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T., Kodama T.,
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; Bacillus/Clostridium gro
    176167
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URSOR (EC 2.4.1.5)
    MW;
                                                                                                                                                                               GLUCAN-BINDING
6.5 X TANDEM RE
                                                                                                                                                                                               GLUCOSYLTRANSFERASE-I.
CATALYTIC (APPROXIMATE).
GLUCAN-BINDING (APPROXIMATE).
                                                                                                                                                                                                                                                                        POTENTIAL.
  (INCOMPLETE).

BCOA66D079351ECF CRC64;
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                                                                                                                                                                                                                                                                                        Signal; Repeat;
                                                                                                                                                                                   TANDEM REPEATS
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                                                                                                                                                                                                                                                                                             Dental caries
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MBL outstation -
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77.78; 77.38;

Score 87; DB 1; Pred. No. 6.2e-06;

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15-DEC-1998 (Rel. 37, L
GLUCOSYLTRANSFERASE-I P
(SUCROSE 6-GLUCOSSE
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REPEAT
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InterPro: IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 19.
Pfam; PF02324; Glyco_hydro_70; 1.
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-i- FUNCTION: PRODUCTION OF EXTRA
                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                 EMBL; M17391; AAC63063.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sobrinus MFe28.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus downei Bacteria; Firmicutes;
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01-JUL-1989 (Rel.
15-DEC-1998 (Rel.
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01-JUL-1989
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                                                                                                                                                              Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-87308014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Nucleotide sequence of a sobrinus MFe28.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ferretti J.J., Gilpin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \vdash
                                                                                                                                                                                                                                                                                                                                                                                              TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIAT AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N)
D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).
                                                                                                                                                                                                                                                                                                                   FORMS OF GLUCANS.
SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES
BINDING PROTEIN FROM S.MUTANS.
                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: SECRETED.
DISEASE: DENTAL CARLES.
MISCELLANEOUS: GTF-I SYNTHESIZES WATER-INSOLUBLE CLICKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S:
WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI
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                                                                                                                                                                                                                                                                                                                                                                                                                                    NCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUTHEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
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lpin M.L., Russell R.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Streptococcus sobrinus).
; Bacillus/Clostridium group;
 177080
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of a glucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
PRECURSOR (EC 2.4.1.5) (GTF-I) (DEXTRANSUCRASE)
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MW;
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                    AC REPEAT
AC REPEAT
AC REPEAT
B REPEAT
AC REPEAT
AC REPEAT
AC REPEAT
B REPEAT
                                                                                                     GLUCONYLTRANSFERASE-I.
CATALYTIC (APPROXIMATE).
GLUCAN-BINDING (APPROXIMATE).
1.25 A, 2 B, AND 5 AC REPEATS
                                                                                                                                                 POTENTIAL.
                    REPEAT.
                                                                                             REPEAT
                                                               REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .Mismatches
                                          REPEAT.
                                                                                    REPEAT.
EPEAT (INCOMPLETE).
B9E86A200868798E CRC64;
                                                                                                                                                           Signal; Repeat; Dental caries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1597
                                                                                                                                                                                                                                                                                                                                AND SOME TO A GLUCAN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
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                                                                                                                                                                                                                                                                                                                                                    E GLUCANS (ALPH
S SYNTHESIZES
SI SYNTHESIZES
                                                                                                                                                                                                                                                                             he EMBL outstat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                  collaboration
                                                                                                                                                                                                                                                                                        outstation
                                                                                                                                                                                                                                                                    in
                                                                                                                                                                                                                                                                                                                                                                                                                                                 BECAUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 17
                                                                       EMBL; M22054; AAA885
EMBL; M17361; AAA885
PIR; JT0345; JT0345.
PIR; C33135; C33135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1303
           Transferase;
SIGNAL
                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene 69:101-109(1988).
                                        Pfam;
                                                                                                                                                                                between
                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ueda S., Shiroza T., Kuran
"Sequence analysis of the
                               Pfam;
                                                  InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70
                                                                                                                                                                                                                                                                                                                                                                                             WEDLINE=87308013;
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-349 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=89137980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TGARTINGQLLYFRANGVQVKG
                                                                                                                                                                                                                                                                   DISEASE: DENTAL CARIES MISCELLANEOUS: GTF-I S
                                                                                                                                                                                                                        FORMS OF GLUCANS.
SIMILARITY: TO OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGAQTIKGQKLYFKANGQQVKG
                              PF01473; CW_binding_1; 7
PF02324; Glyco_hydro_70;
                                                                                                                                                                                                                                                       3-LINKED GLUCOSE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                  Glycosyltransferase;
                                                                                            AAA88592.1;
AAA88589.1;
                                                                                                                                                                                                                                                                                                                                                                                  PubMed=3040685;
S., Kuramitsu H.K.;
 1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=2976010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.7%;
77.3%;
                                                                                                                                                                                                                                                       SYNTHESIZES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22
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Pred.
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STRMU
STANDARD;
GTFC_STRMU
GTFC_STRMU
GTFC_STRMU
STANDARD;
p13470; p05427;
01-NOV-1988 (Rel. 09, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
GLUCOSYLTRANSFERASE-SI PRECURSOR (EC 2.4.1.5) (GTF-SI)
CHYMRANSUCRASE) (SUCROSE 6-GLUCOSYLTRANSFERASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sequence analysis of the gttB gene from Streptococcus mutans.";
"Sequence analysis of the gttB gene from Streptococcus mutans.";
J. Bacteriol. 169:4263-4270(1987).
-!- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT
                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                               European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL I OF THEIR ABILITY TO ADHERE TO SMOOTH SUFFACES AND MEI AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES BINDING PROTEIN FROM S.MUTANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)
SUBCELLULAR LOCATION: SECRETED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE).
                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produ
sen the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                            and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kuramitsu H.K.;
the gtfC gene from Streptococcus mutans GS-5.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus/Clostridium
GLUCOSYLTRANSFERASE-SI
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                                           Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                   It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S WATER-INSOLUBLE GLUCANS (AL
LINKAGES), GTF-S SYNTHESIZES
6-GLUCOSE). GTF-SI SYNTHESIZE
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6.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (N+1).
                                           Repeat; Dental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                            Usage
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                                                                                                                                                                                                                                                                                                                                                 are no rest
its content
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                                                                                                                                                                                                                                                                                                                                                                                                the
                                                                                                                                                                                                                                                                                                                                                                       restrictions
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RESULT 5
GTFS_STRDO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                         Gilmore K.S., Russell R.R., Ferretti J.J.,
"Analysis of the Streptococcus downei gtfS gene, which
glucosyltransferase that synthesizes soluble glucans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P29336;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1993 (Rel. 25, Last annotation update)
GLUCOSYLTRANSFERASE-S PRECURSOR (EC 2.4.1.5) (GTF-S)
(SUCROSE 6-GLUCOSYLTRANSFERASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
DOMAIN
REPEAT
REPEAT
InterPro; IPR003318; Glyco_hydro_70.

Pfam; PF01473; CW_binding_1; 10.

Pfam; PF02324; Glyco_hydro_70; 1.

Transferase; Glycosyltransferase; Signal; Repeat; Dental caries.

SIGNAL 1 36 OR 37 (POTENTIAL).

CHAIN 37 1365 GLUCOSYLTRANSFERASE-S.
                                                                                                                           modified and this statement is not removentities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no resti
                                                                                                    EMBL; M30943; AAA26898.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus downei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                 Infect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-90316665; PubMed-2142479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TGARTINGQLLYFRANGVQVKG
                                                                                                                                                                                                                                                                                       ect. Immun. 58:2452-2458(1990).

FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N) = D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).

ENZYME REGULATION: GLUCAN SYNTHESIS BY GTF-S IS INDEPENDENT OF PRIMER GLUCAN UNLIKE GTF-I.
                                                                                                                                                                                                                              1,6-GLUCOSE).
SIMILARITY: TO OTHER
BINDING PROTEIN FROM
                                                                                                                                                                                                                                                                  MISCELLANEOUS: GTF-S
                                                                                                                                                                                                                                                                                   DISEASE: DENTAL CARIES.
                                                                        A41483; A41483. rPro; IPR002479; CW_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTVTFNGQRLYFKPNGVQAKG
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1253
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1303
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69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 28;
                                                                                                                                                                                                                                 S. MUTANS
                                                                                                                                                                                                                                            GLUCOSYLTRANSFERASES
                                                                                                                                                                                                                                                                      SYNTHESIZES
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GLUCAN-BINDING (APPROXIMA
2.4 A, 1 C AND 1 AC REPEAT
A REPEAT
C REPEAT
C REPEAT
C REPEAT
AC REPEAT
                                                                                                                                                    is not removed.
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Pred.
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REPEAT (INCOMPLETE).
D4B80CBEE0AACE13 CRC64;
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                                                                                                                                                                                                                                                                     WATER-SOLUBLE GLUCANS
                                                                                                                                        noved. Usage by and fo
(See http://www.isb-sib.
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1 AC REPEATS.
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                                                                                                                                                                              restrictions
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Best Local S
Matches 14
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                                                                                                                                                              This SWI
between
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SEQUENCE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Honda O., Kato C., Kuramitsu H.K.;
"Nucleotide sequence of the Streptococcus
the glucosyltransferase-S enzyme.";
J. Gen. Microbiol. 136:2099-2105(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus mutans."; FEMS_Microbiol. Lett. 161:331-336(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-MT4239, MT4245, MT4251, MT4467, AND
MEDLINE-98231643; PubMed-9570124;
Fujiwara T., Terao Y., Hoshino T., Kawabata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecular analyses of glucosyltransferase
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                                                                                                                                                                                                                                 FORMS OF GLUCANS.

SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES AND RINDING PROTEIN FROM S.MUTANS.
                                                                                                                                                                                                                                                                                                                                              MISCELLANEOUS: GTF-I SYNTHESIZES WATER-INSOLUBLE (1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S: WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAY OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIA' AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).
SUBCELLULAR LOCATION: SECRETED.
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                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration
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GLUCAN-BINDING (APPROXIMATE).
4.5 X TANDEM REPEATS.
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EMBL; D88653; BAA26107.1; -.
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EMBL; D88659; BAA26115.1; -.
EMBL; D88669; BAA26115.1; -.
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EMBL; D89979; BAA26121.1; -.
InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco.hydro_70.
Pfam; PF01473; CW_binding_1; 11.
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POTENTIAL.
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                                                                                                                      MT4467).

KKKYTQ -> EKEYTL (IN STRAIN MT4251).

A -> S (IN STRAIN MT4239).

TDQGSEA -> ADKGNDS (IN STRAIN MT4251).

TDQGSEA -> ADKGN (IN STRAINS MT4239 AND MT4245).

TDQGS -> ADKGN (IN STRAINS MT4239 AND MT4245).

E -> K (IN STRAIN MT4245 AND MT4251).

E -> K (IN STRAIN MT4245).

G -> R (IN STRAIN MT4245).

G -> R (IN STRAIN MT4239).

G -> R (IN STRAIN MT4239).

Y -> C (IN STRAIN MT4251).

S -> N (IN STRAIN MT4251).

S -> N (IN STRAIN MT4239).

Y -> C (IN STRAIN MT4251).

S -> N (IN STRAIN MT4251).

S -> N (IN STRAIN MT4251).

S -> N (IN STRAIN MT4251).

O -> P (IN STRAIN MT4251).

O -> P (IN STRAIN MT4245).

K -> T (IN STRAIN MT4245).

N -> D (IN STRAIN MT4245).
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MR 1-3 V ()
S -> A ()
S -> A ()
A ND MT81
A ND MT81
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C -> N ()
D -> N ()
                                Score
Pred.
                                                                       AND MT8148).

R -> G (IN STRAINS MT4239, MT4245, MT4251, MT4467 AND MT8148).

R -> K (IN STRAIN MT4467).

RYYDKNSGNMVYNKVVTLANGRRIGIDRWGIARYY VYR (IN REF. 1).
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MT8148)
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P16154;
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01-FEB-1996
01-NOV-1997
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STRAIN=VPI 10463;
MEDLINE=90129305;
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Clostridium difficile
Bacteria; Firmicutes;
Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                             Sauerborn M., von Eichel-Streiber C.;
"Nucleotide sequence of Clostridium di
Nucleic Acids Res. 18:1629-1630(1990).
                                                                        STRAIN=VPI 10463;
MEDLINE=90221894;
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Virology 229:381-399(1997)
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Ahrens C.H., Russ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Orgyia pseudotsugata multicapsid polyhedrosis virus Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Nucleopolyhedrovirus.
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HYPOTHETICAL 59.0 KDA PROTEIN PRECURSOR (ORF119)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=164623;
                                                                                                                                                                                                                                                                                                                                                                                          1 TGARTINGQLLYFRANGVQVKG
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hedrosis virus genome ";
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HYPOTHETICAL PROTE:
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Best Local S
Matches 12
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EMBL; M30307; AAA23283.1; -.
EMBL; X92982; CAA63564.1; -.
PIR; S08638; S08638.
Interpro; IPR002479; CW_binding.
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Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- DOMAIN: THE C-TERMINAL PART OF TOXIN A CONSISTS OF A 8:
REPETITIVE STRUCTURE. THIS PART OF TOXIN A IS COMPOSED
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                                                                            J. MOI. Biol. 233:414-428(1993).
-I- FUNCTION: KILLS CELLS. DOC AND STABILIZE PLASMID NUMBER BY INC
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01-NOV-1995 (Rel. 32, La
DEATH ON CURING PROTEIN.
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  This
                                                                                                                          SEQUENCE FROM N.A.

MEDLLNE=94016561; PubMed=8411153;

MEDLLNE=94016561; PubMed=8411153;

Lehnherr H., Maguin E., Jafri S., Yarmolinsky M.B.;

Plasmid addiction genes of bacteriophage P1: doc, which causes

"Plasmid addiction genes of bacteriophage P1: doc, which causes
death on curing of prophage, and phd, which prevents host death
                                                                                                                                                                                                                                                                                                Q06259;
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J. Mol. Biol ~~~
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Viruses; dsDNA viruses,
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DISEASE: CLOSTRIDIUM DIFFICILE PRODUCES TWO TOXINS, AN DISEASE: CLOSTRIDIUM DIFFICILE PRODUCES TWO TOXINS, AND CYTOTOXIN B. ONLY AFTER THE ENTERAL DELIVERY OF THE ENTEROTOXIN A MAY THE CHARACTERISTIC DISEASE CALLED PSEUDOMEMBRANOUS COLITIS BE INDUCED.
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         IDENTIFICATION OF MEDLINE-96224025; Parks C.L., Shenk The serotonin la
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                                                                                                  STRUCTURE BY NMR OF 654-684
MEDLINE=97218212; PubMed=906
Narayan V.A., Kriwacki R.W.,
                                                                                                                                                                                                                                           Kadonaga J.T., Carner K.R., "Isolation of cDNA encoding analysis of the DNA binding
                                                                                                                                                                                                                                                                                                            MEDLINE-20545561; PubMed-10973950;
MEDLINE-20545561; PubMed-10973950;
Takahara T., Kanazu S., Yanagisawa S.
"Heterogeneous Sp1 mRNAs in human Hep
homotypic trans-sp11cing.";
J. Biol. Chem. 275:38067-38072(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-AUG-1988 (Rel. 08, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation updat
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Jackson S.P., Tji
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                                                                                                                                                  Cell 55:125-133(1988).
                                                                                                                                                           Jackson S.P., Tjian R.;
"O-glycosylation of eukaryotic transcription for mechanisms of transcriptional regulation
                                                                                                                                                                                                                                Cell 51:1079-1090(1987).
                                                                                                                                                                                                                                                                                                                                                                                               Submitted
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by non-profit institutions as long as i
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126 AA;
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                                SEROTONIN 1A RECEPTOR PubMed=8626793;
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         receptor
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RESULT 11
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01-APR-1993
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Q01714;
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ZN_FING
ZN_FING
MEDLINE-93010958; PubMed=1356762; Imataka H., Sogawa K., Yasumoto K., Kikuch Kobayashi A., Hayami M., Fujii-Kuriyama Y. "Two regulatory proteins that bind to the (BTE), a GC box sequence in the promoter r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR00082; Znf-C2H2.

Pfam; PF00096; Zf-C2H2; 3.

SMART; SM00355; ZnF_C2H2; 3.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.

PROSITE; PS0157; ZINC_FINGER_C2H2_2; 3.

Transcription regulation, Activator; Zinc-finger; Metal-binding; Nuclear protein; Repeat; Glycoprotein; 3D-structure DNA-binding; Nuclear protein; Repeat; Glycoprotein; 3D-structure
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                                                                                                                                                                                       Rattus norvegicus (Rat)
Eukaryota; Metazoa; Chou
Mammalia; Eutheria; Rode
MCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDB; 1SP1; 21-APR-97.
PDB; 1SP2; 21-APR-97.
TRANSFAC; T00759; -.
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                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              TRANSCRIPTION
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SUBCELLULAR LOCATION: NUCLEAR.
SUBCELLULAR LOCATION: NUCLEAR N-ACETYLGLUCOSAMINE SIDE CHAINS.
PTM: O-GLYCOSYLATED; CONTAINS N-ACETYLGLUCOSAMINE SIDE CHAINS.
SIMILARITY: BELONGS TO THE SP1 FAMILY OF C2H2-TYPE ZINC-FINGER
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708 ZINC FINGERS.
650 C2H2-TYPE.
680 C2H2-TYPE.
708 C2H2-
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PIR; JS0747; JS0747.

HSSB; P08047; ISP1.

TRANSFAC; T00754; -.

InterPro; IPR00082; Enf-C2H2; 3.

Pfam; PF00096; Zf-C2H2; 3.

PRINTS; PR00048; ZINCFINGER.

SMART; SM00355; ZRF-C2H2; 3.
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PROSITE: PS50157; ZINC_FINGER_C2H2_2; 3.
Transcription regulation; Activator; Zinc-finger; Metal-binding; DNA-binding; Nuclear protein; Repeat; Glycoprotein.
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EMBO J. 11:3663-3671(1992).
-i- FUNCTION: BINDS TO GC BOX PROMOTERS
-CTIVATES MRNA SYNTHESIS FROM GENES
                                        Nature 392:353-358(1998).
-!- CATALYTIC ACTIVITY: 4-CARBOXYMETHYLENEBUT-2-EN-4-OLIDE + H(2)0
                                                                                                     MEDLINE=98196666; PubMed=9537320;
Deckert G., Warren P.V., Gaasterland T., Young W.G., Le
Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PUTATIVE CARBOXYMETHYLENEBUTENOLIDASE (EC 3.1.1.45) (DIENELACTONE
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Bacteria; Aquificales;
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                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo
                                                                                                                                                                                                                                                                   Behammer W., Shao Z., Mages W., Rachel R., Stetter K.O., Schmitt R.; Schmitt R.; "Flagellar structure and hyperthermophily: analysis of a single flagellin gene and its product in Aquifex pyrophilus."; J. Bacteriol. 177:6630-6637(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                      InterPro; IPR002925; DLH.
InterPro; IPR002925; Est_lip_thioest_actsite
Pfam; PF01738; DLH; 1.
SEQUENCE 231 AA; 26140 MW; C55E408839920;
                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                    EMBL; U17575; AAA88922.1; -.
                                                                                                                                                                                                                                                                                                                              MEDLINE-96062250;
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                                                                                                                                                                                                                                                                                                                                                                                      Aquifex pyrophilus.
Bacteria; Aquificales;
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ASIALOGLYCOPROTEIN I
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058723;
20-AUG-2001
20-AUG-2001
20-AUG-2001
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STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Eleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Reich C.I.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.D., Reich C.I.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.D., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woose C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                  LECI_MOUSE P24721;
                                                                                                                                                                                                                                                                                                                                                                            EMBL; U67573;
REBASE; 3894;
TIGR; MJ1327;
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                                                                                                                                                                                                                                                                                                                             SEQUENCE 245 AA;
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-i- CATALYTIC ACTIVITY: RECOGNIZES THE DOUBLE-STRANDED
                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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NCBI_TaxID=2190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                            Hydrolase; Endonuclease; Nuclease; Restriction system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (R.MJAIV).
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1 (Rel. 40, Last a
1 (Rel. 40, Last a
             (Rel. 21, Created)
(Rel. 21, Last sequence update)
(Rel. 39, Last annotation update)
PROTEIN RECEPTOR 2 (HEPATIC LECTIN
                                                                                                                                                                                                                                                Conservative
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PIR; S13165; S13165.
HSSP; P06734; IXJE.
MGD; MGI:88082; Asgr2.
Interpro; IPR001304; lectin_c.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
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PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Lectin; Glycoprotein; Receptor; Endocytosis; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Biochim. Biophys. Acta 1087:259-261(1990).

-i- FUNCTION: MEDIATES THE ENDOCYTOSIS OF PLASMA GLYCOPROTEINS TO WHICH THE TERMINAL SIALIC ACID RESIDUE ON THEIR COMPLEX CARBOHYDRATE MOIETIES HAS BEEN REMOVED. THE RECEPTOR RECOGNIZES TERMINAL GALACTOSE AND N-ACETYLGALACTOSAMINE UNITS. AFTER LIGAND BINDING TO THE RECEPTOR, THE RESULTING COMPLEX IS INTERNALIZED AND TRANSPORTED TO A SORTING ORGANELLE, WHERE RECEPTOR AND LIGAND ARE DISASSOCIATED. THE RECEPTOR THEN RETURNS TO THE CELL MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - PART - 
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STRAIN=C57BL/6; TISSUE=Liver;
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[1]
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-!- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN HEPATIC PARENCHYMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
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    153
                                                                             4 RTINGQLLYFRANGVQ 19
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RTLTCQLAYFQSNGTE 168
                                                                                                                                                      Similarity
8; Conserv
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298
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Pred. No. 4.1;
4; Mismatches
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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1 TGARTINGQLLYFRANGVQVKG 22
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	80	7	6	5	4	w	2	<b>—</b>	Result
66	68	68	72	72	72	72	73	75	75	76	78	80	82	86	87	90	90	90	Score
58.9	60.7	60.7	64.3	64.3	64.3	64.3	65.2	67.0	67.0	67.9	69.6	71.4	73.2	76.8	77.7	80.4	80.4	80.4	Query Match
1577	1449	563	1577	1508	1508	1477	1449	1338	1290	1590	1390	1518	1599	1455	1590	1455	1455	1455	Length
ν	2	2	N	N	2	2	2	2	N	N	2	N	2	Ν	2	2	N	ν	DB
Q55265	068542	Q54447	Q54178	Q9EZHS	052224	Q9L466	Q55264	Q9WXJ4	Q48756	Q55263	069385	200600	Q00599	069391	Q59983	069397	069388	069382	ID
Q55265 streptococc	068542 streptococc	Q54447 streptococc	Q54178 streptococc	Q9ezh5 leuconostoc	052224 leuconostoc	Q91466 leuconostoc	Q55264 streptococc	Q9wxj4 streptococc	. Q48756 leuconostoc	Q55263 streptococc	069385 streptococc	Q00600 streptococc	Q00599 streptococc	069391 streptococc	Q59983 streptococc	069397 streptococc	069388 streptococc	069382 streptococc	Description

069388

## ALIGNMENTS

Дb	Qu Be	SQ	ΚW	DR DR	DR	DR	DR	RL	RT	RT.	RA	RA	RX	RC	RP	RN	OX.	8	8	SO	GN	DE	DT	DŢ	Δī	AC	ID	RESULT 069382
1 TGARTINGQLLYFRANGVQVKG 22       :                1329 TGARVVNGQRLYFKSNGVQAKG 1350	Query Match 80.4%; Score 90; DB 2; Length 1455; Best Local Similarity 72.7%; Pred. No. 9.2e-06; Matches 16; Conservative 3; Mismatches 3; Indels 0; Gaps 0;	SEQUENCE 1455 AA; 162969 MW; 27D4D3A1EECA2939 CRC64;	Transferase.	Pfam; PF02324; Glyco_hydro_70; 1.	Interpro: IPRUJ3318; Glyco_hydro_70.		EMBL; D88652; BAA26102.1;	FEMS Microbiol. Lett. 161:331-336(1998).	9	"Molecular analyses of glucosyltransferase genes among strains of		Fujiwara T., Terao Y., Hoshino T., Kawabata S., Ooshima T., Sobue S.,	MEDLINE=98231643; PubMed=9570124;	STRAIN=MT83 48;	SEQUENCE FROM N.A.	[4]	NCBI_TaxID=1209;		Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;	Streptococcus mutans.	GTFC.		(TrEMBLrel. 17, Last	(TrEMBLrel 07,	01-AUG-1998 (TremBLrel. 07, Created)		O69382 PRELIMINARY; PRT; 1455 AA.	LT 1 82

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SEQUENCE 1
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InterPro; IPR003318; Glycc_hydro_70.
Pfam; PF01473; CW_binding_1; 9.
Pfam; PF02324; Glyco_hydro_70; 1.
                                                                                                                                                                                    Streptococcus mutans."; FEMS Microbiol. Lett. 161:331-336(1998). EMBL; D89978; BAA26120.1; -
                                                                                                                                                                                                                                     Kimura S., Hamada S.;
"Molecular analyses of glucosyltransferase
                                                                                                                                                                                                                                                                  MEDLINE-98231643; PubMed-9570124; Fujiwara T., Terao Y., Hoshino T.,
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InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 10.
Pfam; PF02324; Glyco_hydro_70; 1.
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FEMS Microbiol. Lett. 161:331-336(1998).
EMBL; D88658; BAA26110.1; -
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Kimura S., Hamada S
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Score 90; DB
Pred. No. 9.2e
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Interpro; IPR003318; Glyco_hydro_70.
Interpro; IPR003318; Glyco_hydro_70.
If am; PF01473; CW_binding_1; 16.
Pfam; PF02324; Glyco_hydro_70; 1.
Signal; Transferase; Glycosyltransferase.
SIGNAL 1 38
CHAIN 1 39 1590
SEQUENCE 1590 AA; 175955 MW; C3C83A57CF
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01-AUG-1998
01-JUN-2001
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01UCOSYLTRANSFERASE-I PRECURSOR (EC 2.4.1.5) (DEXTRANSUCRASE) (SUCROSE 6-GLUCOSYLTRANSFERASE).
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DNA Seq. 4:19-27(1993).

-!- CATALYTIC ACTIVITY: SUCROSE + ((1,6)-ALPHA-D-GLUCOSYL)(N)
FRUCTOSE + ((1,6)-ALPHA-D-GLUCOSYL)(N+1).

EMBL; D13858; BAA02976.1; -.
                                                                 STRAIN=MT4251;
MEDLINE=98231643; PubMed=9570124;
Fujiwara T., Terao Y., Hoshino T.,
Kimura S., Handa S.,
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01-JUN-2001 (TrEMBLrel.
GLUCOSYLTRANSFERASE-SI.
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STRAIN=OMZ176;
MEDLINE=94146405; PubMed=8312602;
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                           Streptococcus mutans."; FEMS Microbiol. Lett. 161:331-336(1998).
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                EMBL; D88661; BAA26114.1;
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 InterPro;
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MW; C3C83A57CF3C2B0E CRC64;
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STRAIN=ATCC 25975;

STRAIN=93381463; PubMed=8371114;

Giffard P.M., Allen D.M., Milward C.P., Simpson C.L., Ji.

"Sequence of the gtfK gene of Streptococcus Salivarius evolution of the gtf genes of oral streptococci.";

"on Microbiol. 139:1511-1522(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q00599;
01-NOV-1996
01-NOV-1996
01-JUN-2001
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                                                     SIMILAR
SIMILAR
SEQUENCE
                                                                                                                                                                                                                                                        AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

-! CATALYTIC ACTIVITY: SUCROSE + ((1,6)-ALPHA-D-GLUCOSYL)(N)
FRUCTOSE + ((1,6)-ALPHA-D-GLUCOSYL)(N+1).

-! SUBCELLULAR LOCATION: EXTRACELLULAR.

-! DISEASE: DENTAL CARIES.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLREL. 17, Last annotation update)
01-JUN-2001 (TrEMBLREL. 17, Last annotation update)
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SEQUENCE 1
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                                                                                                                                                  Pfam;
                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                      glucosyltransferase genes in Streptococcus salivarius J. Gen. Microbiol. 137:2577-2593(1991).
-i- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THE PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL I
                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=ATCC 25975;
MEDLINE=92148377; PubMed=1838391;
Giffard P.M., Simpson C.L., Milward C.P., Jacques N.A.;
"Molecular characterization of a cluster of at least two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus salivarius
                                                                                                           Transterase;
SIGNAL
                                                                                                                                                         InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                               -!- SIMILARITY: TO REGIONS OF BARLEY AND ALPHA AMYLASES AND RABBIT GLYCOGEN PH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus
                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                          THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE
                                                                                                                                                                                        Z11872; CAA77898.1;
Z11873; CAA77901.1;
M64111; AAA26897.1;
                                                                                                                   PF01473; CW_binding_1; 14.
PF02324; Glyco_hydro_70; 1.
ferase; Glycosyltransferase; Signal; Repeat; Dental caries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity 68.
15; Conservative
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                                                      867
1132
1599
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                                                      Α,
                                                                                  1599
967
                                                                  1219
73.
77.
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                                                      176480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 28;
 . 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .88;
                                                   POTENTIAL
GLUCOS'LTRANSFERASE:
TO ALPHA-AMYLASES.
TO GLYCOGEN PHOSPHOR:
TO GLYCOGEN PHOSPHOR:
0 MW; 24B77869E152B707
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Pred.
 Score
Pred.
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                                                     GLYCOGEN PHOSPHORYLASE
24B77869E152B707 CRC6
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 No.
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No. 4e-05;
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DB 2;
0.0002;
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             Length 1599
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25975 and
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                                                                                                                                                                      Query Match
Best Local Similarity
Matches 16; Conserv
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                               069385;
01-AUG-1998
01-AUG-1998
01-JUN-2001
                                                                                                                                                                                                                          REPEAT
REPEAT
SEQUENCE
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          GTFC.
Streptococcus mutans
                                                                                                                             1383
                                                                                                                                                                                                                                                                    REPEAT
REPEAT
                                                                                                                                                                                                                                                                                          DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z11873; CAA77900.1; -. EMBL; M64111; AAA26896.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                         glucosyltransferase genes in Streptococcus salivarius ATCC 25975.";
J. Gen. Microbiol. 137:2577-2593(1991).
-i- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Giffard P.M., Simpson C.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTFJ.
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                     GLUCOSYLTRANSFERASE-SI.
                                                                         069385
                                                                                                                                                                                                                                                                                                                         Pfam; PF01473; CW_binding_1; 13
Pfam; PF02324; Glyco_hydro_70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92148377; PubMed=1838391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus salivarius
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                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              iffard P.M., Simpson C.L., Milward C.P., Jacques Molecular characterization of a cluster of at lea
                                                                                                                                                1 TGARTINGQLLYFRANGVQVKG
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                                                                                                                                                                                                                                                                                                                                                                                      AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

CATALYTIC ACTIVITY: SUCROSE + ((1,6)-ALPHA-D-GLUCOSYL)(N)
FRUCTOSE + ((1,6)-ALPHA-D-GLUCOSYL)(N+1).

SUBCELLULAR LOCATION: EXTRACELLULAR.

DISEASE: DENTAL CARIES.
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                                                                                                                             TGAQVINGQHLYFNADGSQVKG
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                            (TrEMBLrel.)
(TrEMBLrel.)
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                                                                         PRELIMINARY;
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1338
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72.7%;
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17, Last annotation update)
EC 2.4.1.5) (GTF) (DEXTRANSUCRASE).
                                                                                                                                                                                                                                                                                                                        _70;
                              Created)
Last sequence
Last annotation
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PEPEAT 2.
PEPEAT 3.
PEPEAT 4.
PEPEAT 5.
PEPEAT 6.
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                              sequence update)
annotation update)
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least two
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RESULT
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ID Q5 263
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Best Local
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Q55263;
Q1-NOV-1996 (TrEMBLrel. 01, C
Q1-JAN-1998 (TrEMBLrel. 05, I
Q1-JUN-2001 (TrEMBLrel. 17, I
GLUCOSYLTRANSFERASE GTF-I.
                              Q48756;
Q48756;
Q1-NOV-1996;
Q1-NOV-1996;
Q1-JUN-2001;
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InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 7.
Pfam; PF02324; Glyco_hydro_70; 1.
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Streptococcus mutans.";
PPMS Microbiol. Lett. 161:331-336(1998).
DEXTRANSUCRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                      Transferase.
SEQUENCE 1590 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus.
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SEQUENCE 1
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Fujiwara T., Terao Y., Hoshino T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1310;
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EMBL; D88655; BAA26106.1;
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"Molecular analyses of glucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-MT4245;
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nes 15; Conservative
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31 TGAQTVGKQKLYFEANGEQVKG
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15; Conser
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(TrEMBLrel.)
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01-NOV-1999
01-NOV-1999
01-JUN-2001
                                                                                                                                         Pfam; PF
Pfam; PF
Plasmid.
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Pfam; PFC
SEQUENCE
                                                     1207
                                                                                                                                                                                                                                                                                                     GTFS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "S.Crizetus glucosyltransferase(gtfS and gtfT) genes.";
"S.Crizetus glucosyltransferase(gtfS and gtfT) genes.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AB026123; BAA77236.1; -.
HSSP; P06278; 1VJS;
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InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 11.
Pfam; PF02324; Glyco_hydro_70; 1.
SEQUENCE 1290 AA; 145590 MW; 355
                                                                                                                                                 InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 10.
Pfam; PF02324; Glyco_hydro_70; 1.
                                                                                                                                                                                                                               STRAIN-HS-6;
                                                                                                                                                                                                                                                                  Streptococcus
                                                                                                                                                                                                                                                                          Bacteria;
                                                                                                                                                                                                                                                                                  Plasmid pAM1.
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Bacteria; Firmicutes; Baci
                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                         NCBI_TaxID=1333;
                          12
                                                                     1 TGARTINGQLLYFRANGVQVKG
                                                                                                                                                                                                                                                                                                                                                                                                                    1 TGARTINGQLLYFRANGVQVKG
                                                    TGSQTIAGQKVFFQPNGVQVKG
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15; Conserv
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                                                                                       Conservative
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63.6%;
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68
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 1368
                                                                                                      InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 14.
Pfam; PF02324; Glyco_hydro_70; 1.
Transferase; Glycosyltransferase.
SEQUENCE 1477 AA; 164886 MW; E6F
                                                                                                                                                                          Arguello-Morales M.A., Remaud-Simeon M., Pizzut S., Sarc Willemot R.M., Monsan P.;
"Sequence analysis of the gene encoding alternansucrase, glucosyltransferase from Leuconostoc mesenteroides NRRL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ250172; CAB76565.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal; Transferase.
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InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 8.
Pfam; PF02324; Glyco_hydro_70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=95122197; PubMed=7822030;
Simpson C.L., Giffard P.M., Jacqu
"Streptococcus salivarius ATCC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus.
NCBI_TaxID=1304;
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                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=NRRL B-1355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coding for primer-independent glucosyltransferases. Infect. Immun. 63:609-621(1995).
EMBL; L35495; AAC41412.1; -.
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Streptococcus salivarius.
                                                                                                                                                                                                                                                                                     NCBI_TaxID=1245;
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TGLVNINGNLKYFQANGRQVKG
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68.2%;
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                                          Score 72; DB Pred. No. 0.00
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CC 25975 possesses at least
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W; DD62F07306E86A46 CRC64;
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01-JUN-1998 (TrEMBLrel. 0
01-JUN-1998 (TrEMBLrel. 0
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLREL. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9EZH5;
01-MAR-2001
01-MAR-2001
01-JUN-2001
                                                                                                                                            Kim H.-S., Kim D., Ryu H.-J., Robyt J.F.;
"Leuconostoc mensenteroides B-742CB, a dextransucrase gene.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF294469; AAG38021.1;
-InterPro; IPR002479; CW_binding.
InterPro; IPR00318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 14.
Pfam; PF01473; CW_binding_1; 14.
Pfam; PF02324; Glyco_hydro_70; 1.
SEQUENCE 1508 AA; 168542 MW; E2FCFA0F87AE4F3A CRC64;
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EMBL; AF030129; AAB95453.1; -
InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 14.
Pfam; PF02324; Glyco_hydro_70; 1.
Transferase; Glycosyltransferase.
SEQUENCE 1508 AA; 168511 MW; E70CECB57A70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=NRRL B-1299;
MONChOis V., Remaud-Simeon M., Monsan P., Willemot R.M.;
FEMS Microbiol. Lett. 0:0-0(1998).
-i- CATALYTIC ACTIVITY: SUCROSE + ((1,6)-ALPHA-D-GLUCOSYL)(N)
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Bacteria: Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
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NCBI_TaxID=1245;
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TGARTINGQLLYFRANGVQVKG
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                                         l Similarity
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TrEMBLrel.
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irmicutes; Bacillus/Clostridium
                                           Conservative
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17, Last annotation update)
2.4.1.5) (DEXTRANSUCRASE) (
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Pred.
1; Mis
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Pred. No. 0.00
1; Mismatches
22
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                                                                                   Length 1508;
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Db 1399 TGLVNINGNLKYFQANGRQVKG 1420

Search completed: March 27, 2002, 14:26:03 Job time: 1675 sec

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Result
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM protein - protein search, using sw model
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119
                                                                                                                                                                                                                                                                                                                                                                                    SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:

SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:

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SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:

SIDSB/gcgdata/geneseq/geneseqp/AA1987.DAT:

SIDSB/gcgdata/geneseq/geneseqp/AA1987.DAT:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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1592
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                 AAG09844
AAG09844
AAM43544
AAY67414
AAG09941
AAR65965
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AAB10667
AAY60021
                                                                                                                                  AAB36552
                                                                                                                                                                                         AAR32925
                                                                                                                                                                                                                                                                                  SUMMARIES
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                                                                                                                          Glucosyltransferea
Alpha-D-glucosyltr
L. mesenteroides a
Lawsonia intracell
                               Arabidopsis thalia
Arabidopsis thalia
Human polypeptide
Arabidopsis aldehy
Arabidopsis thalia
                                                                                                                                                                                                                          Description
                   niveum
endometrium
                   GAPDH
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	148	19	298		42	<b>4</b> 5
Smi	93	17	259	ū	42	44
frc	AAW89935	20	239	Ġ	42	
3	AAW90021	20	236	<u>ب</u>	42	42
Arabidopsis thalia	AAG60585	21	189	5	42	41
Arabidopsis thalia	AAG60586	21	185	5	42	40
Human Fc gamma rec	AAP90061	10	178	5	42	39
Arabidopsis thalia	AAG60587	21	174	5	42	38
Œ	AAB79865	22	123		42	37
	AAM40156	22	390	<u>ب</u>	Ñ	36
Human polypeptide	AAM41942	22	325	5.	42.5	35
acid s	AAB19343	21	2485	9	43	34
PTPL1 p	AAY90272	21	2466	σ.	43	33
cellular	AAW75999	19	2466	რ	43	32
Human protein tyro	AAR71498	16	2466	σ.	43	31
mophi	AAW75420	20	1195		43	30
Ŧ	AAY05368	20	335	6.	43	29
Ψ	AAY07036	20	335	σ.	43	28
	AAG64817	22	327	σ.	43	27
Arabidopsis thalia	AAG26414	21	194	ა	43	26
Arabidopsis thalia	AAG53892	21	193		43	25
S	AAG53893	21	170	6.	43	24
	AAG26415	21	170	6.	43	23
ŝ	AAG53894	21	126	ა	43	22
is thal	AAG26416	21	126	σ.	43	21
		21	384	7.	44	20
dis c	œ	22	220	7.	44	19
	2844	21	206	7.	44	18
sis thali	2844	21	161	7.	44	17
	486	21	62	.7	44	16
Fusarium oxysporum	15	12	385	7.	45	15
mino acid sequen	23	20	236	37.8	45	14
. pneumoniae	352	20	336	ω.	46	13
C glutamicum prote	AAG90817	22	199	8	46	12

#### ALIGNMENTS

RESULT AAR32925

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Claim 13; Page 15; 29pp; Japanese
                                                                                                                                                                                                 GT-1; Streptococcus; dental; caries
                                                                                                                                                                                                                   Glucosyltransferease
                       DNA sequence glucosyl:transferase-I - comprises Streptococcus sobrinus DNA sequence with at least one nucleotide added or deleted
                                                          WPI; 1993-079449/10.
N-PSDB; AAQ37760.
                                                                                                                                               02-FEB-1993.
                                                                                                                                                                                 Streptococcus sobrinus
                                                                                                             25-JUL-1991;
                                                                                                                                                                JP05023188-A.
                                                                                                                                                                                                                                  28-JUN-1993 (first entry)
                                                                                                                                                                                                                                                      AAR32925;
                                                                                                                                                                                                                                                                      AAR32925 standard; Protein; 1592 AA
                                                                                   (FUKU/) FUKUI I.
(KATO/) KATO K.
                                                                                                                              25-JUL-1991;
                                                                                                              91JP-0186592
                                                                                                                              91JP-0186592
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RESULT
AAR91047
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Best Local
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                The sequence represents an alpha-D-glucosyltransferase from Streptococcus salivarius. The enzyme is primer-independent, and produces soluble glucan from sucrose. A gene encoding the enzyme may be cloned and expressed in Escherichia coli using a subclone of phage lambda-Cl3, e.g. plasmid pGSG501 or plasmid pGSG502. The DNA may also be expressed in a transgenic plant, to improve the level of stored carbohydrate in a pasture plant which normally contains low levels, or to prevent degradation of stored carbohydra during plant senescence. Dextran may be isolated from the plant, functions as a food binder or pharmaceutical additive. Primer independent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alpha-D-glucosyltransferase; primer-independent; soluble gl
sucrose; transgenic plant; cloning; Escherichia coll;
phage lambda-Cl3; vector; plasmid pGSG501; plasmid pGSG502;
gene transfer; crop improvement; storage carbohydrate; past
feedstuff; senescence; dextran; binder; food; pharmaceutica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The DNA sequence from Streptococcus sobrinus strain 6715 encodes glucosyltransferase-I (and mutants). The DNA was obtd. by treath, s. sobrinus 6715 with mutanolysin, extracting the chromosomal DNA, partially digesting with Sau3AI and fractionating on agarose gel. The 3-5 kbp fragment was ligated into pUC18 and E. coli JM109 transformed with it. A GT-1 expressing clone was isolated and sequenced. The clone may be used in the development of a drug for
                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                    Plants contg. new bacterial DNA encoding glucosyl transferase activity - retain higher levels of stored carbohydrate(s) in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GIFF/)
                                                                                                                                                                                                                                                                                                                  readily
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-FEB-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alpha-D-glucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dental caries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SIMP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ANDHLSILEAWSDNDTPYLHD 21
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DB; AAT13139.
                                                                                                                                                                                                                                                                      4; Page 16-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GIFFARD P
JACQUES N
SIMPSON C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                               digestible by
    that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jacques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   salivarius strain ATCC 25975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94AU-0007643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95WO-AU00527
    enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   r > 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.8%;
85.7%;
                                                                                                                                                                                                                                                                    31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NA,
                                                                                                                                                                                                                                                                                                                  ruminants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Simpson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 108;
Pred. No. 1
  functional in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 14;
1.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
f stored carbohydrate
d from the plant, for
Primer independence
ants. The glucan is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  soluble glucan;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1592;
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Query Match Best Local S Matches 11

l Similarity 11; Conserv

Conservative

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9

Indels

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Gaps

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Length 2057;

50 55

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Score 60; DB 1 Pred. No. 2.8; 3; Mismatches

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RESULT
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Best Local (
                                                                                                                                  carbohydrate) and/or fructose by secreting the enzyme into a saccharose-containing culture medium. Alternatively, the enzyme is contacted with a saccharose-containing solution. The alternan and/or fructose is then isolated from the medium. Cosmetic products or foodstuffs containing alternan can be produced. Recombinant production alternan sucrase is advantageous as it provides a cost effective mean alternan sucrase is advantageous as it provides a cost effective mean
                                                                                                                                                                                                                                                                           This invention describes a novel nucleic acid molecule (I) alternan sucrase (E.C. 2.4.1.140 - an enzyme, that belongs glucosyltransferase group) The recombinant, purified altern gene is useful for the fermentative production of alternan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PLAN-)
                                                                  producing fructose for high fructose containing syrups, production which previously has been achieved by costly production from maize starch. This sequence represents the Leuconostoc mesenteroides altered the content of the content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    poorly degraded in plants but easily degraded by bacteria of grazing livestock.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                             Claim la;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding alternan sucrase protein a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB10667
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                                                                                                                 producing fructose for high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kossmann J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leuconostoc mesenteroides
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                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the Lawsonia intracellularis flagellar hook protein FlgE. The present invention describes an isolated or recombinant polypeptide (I) that comprises, minics or cross-reacts with a B- or T-cell epitope of a FlgE (flagellar hook) polypeptide from a Lawsonia spp. (I) has antibacterial activity, and induces a specific humoral immune response. (I) are used as antigens in vaccines to prevent correct infection by Lawsonia, in birds and animals, especially pigs, to raise specific antibodies (Ab) and to defect past or present corrimensologically cross-reactive species, ato for identification of cepitopes in FlgE. Vectors that contain nucleic acids (II) encoding (I) are useful in genetic vaccines, and fragments of (II) are useful cas primers or probes for detecting L. intracellularis or related microorganisms, in hybridisation or amplification assays.
                                                                                       Query Match 42.9
Best Local Similarity 47.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; Page 87-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New immunogenic Lawsonia FlgE peptide, its nucleic acid and antibody, useful in vaccines and diagnosis of Lawsonia infections, particularly
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Ankenbauer
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(AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
(PIGR-) PIG RES & DEV CORP.
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				fragment SEQ ID NO: 7934. 11 transduction pathway; metabolic pathway; mapping; gene expression control; promoter;
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RESULT
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 Human; antiarthritic; antirheumatic; antiproliferative; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic; neuroprotective; antiallergic; hepatotropic; antidiabetic;
                                                                            Human
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16-MAR-2000;
17-MAR-2000;
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antiparasitic; cardiant; gene therapy; cancer; immune disorder;
cardiovascular disorder; neurological disease; infection; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or ameliorating medical conditions e.g. by protein or gene therapy. The genes were isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (antiagonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, croth's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischammiae.
                                                                                     06-JAN-2000
                                                                                                                                           Arabidopsis sp
                                                                                                                                                                                      Arabidopsis; plant plastid; acetyl CoA synthetase; E3 subunit; ACS; plant plastidic pyruvate dehydrogenase; pPDH; ATP citrate lyase; ACL; pyruvate decarboxylase; PDC; aldehyde dehydrogenase; ALDH; acetyl COA; fatty acid; flavonoid; enzyme; phytochemical; pyruvate decarboxylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epilepsy; and (f) infecti
and parasitic infections.
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the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acids treating and/or preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-DEC-2000;
05-JAN-2001;
                          26-JUN-1998;
                                                       25-JUN-1999;
                                                                                                                  WO200000619-A2
                                                                                                                                                                          acetyl CoA hydrolase;
                                                                                                                                                                                                                                                                  Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     itis; (c) cardiovascular disorders such as myocardial ischaemias; wound healing; (e) neurological diseases e.g. cerebral anoxia and lepsy; and (f) infectious diseases such as viral, bacterial, funga
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                                                                                                                                                                                                                                                                  aldehyde dehydrogenase (ALDH)-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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2001US-0259678.
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                           98US-0090717
                                                       99WO-US14382
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Pred. No. 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention provides nucleic acids encoding Arabidopsis plastidic CC acetyl COA synthetase (ACS), various subunits (specifically the E3 CC subunit) of plant plastidic pyruvate dehydrogenase (pPDH), the A and B subunits of a plant ATP citrate lyase (ACL), Arabidopsis pyruvate decarboxylase (PDC), Arabidopsis aldehyde dehydrogenase (ALDH), specifically ALDH-2 and ALDH-4. The polypeptides can be expressed by specifically ALDH-2 and ALDH-4. The polypeptides can be expressed by standard recombinant methodology. The ACS, pPDH, ACL, PDC and ALDH CC polypeptides, methods and nucleic acid molecules of the invention are CC used to alter the level of acetyl COA is explant or plant cell, tissues CC or organs. A decrease in acetyl COA is expected to affect the biosynthesis of very long chain fatty acids and flavonoids. The enzymes me used to produce acetyl COA phytochemicals (plastidic ACS, pDDH, ACL, CC pyruvate decarboxylase, acetyl COA phytochemicals (plastidic ACS, pDDH, ACL, CC dehydrogenase and aldehyde dehydrogenase are involved in the biosynthesis of acetyl COA.
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25.FEB-1999
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                                                                                                                                                                                                                                                                                                                                                       AAG09941 standard;
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                                                                                                                                                                                                                                   Protein identification;
hybridisation assay; gen
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                                                                                                                                                                                                Arabidopsis thaliana.
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99US-0127462.
99US-0128234.
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                                                                                                                                                                                                                                                                                                                                                       Protein; 195
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                                                                                                                                                                                                                                     genetic
                                                                                                                                                                                                                                    signal transduction pathway; metabolic
netic mapping; gene expression control;
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Fatland
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Pred.
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Lutziger I,
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promoter;
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04-MAY-1993;
17-MAY-1993;
                                                                                                               Kocher HP,
Weber G;
New nucleic acid encoding eukaryotic alanine racemase - and related vectors, host cells and recombinant enzyme, useful producing cyclosporin derivs. or increasing cyclosporin pro
                                                                            WPI;
                                                                                                                                                                  (SANO
                                                                                                                                                                                                                                                                                                                                                                                                                             Tolypocladium niveum ATCC 34921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alanine-racemase; glyceraldehyde-3-phosphate-dehydrogenase; GAPDH; cyclosporin; immunosuppressive.
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SANDOZ PATENT GMBH.
SANDOZ-ERFINDUNGEN VERW GES MBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
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28-SEP-1999
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990S-014433 990S-014433 990S-014483 990S-014484 990S-0145086 990S-0145086 990S-0145089 990S-0145089 990S-014518 990S-014518 990S-014591 990S-014720 990S-014902 990S-0151086 990S-0151086 990S-0151086 990S-0155086 990S-0158086 990S-0158029 990S-0158029 990S-0158029 990S-0158029

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a fragment of the glyceraldehyde-3-phosphate-dehydrogenase (GAPDH) gene from Penicillium chrysogenum. A 2.2 kb fragment was identified (AAQ78277) and cloned in pUC18 to give pGT1. A 665 bp HindIII-HindII fragment of this was used to screen cosmid DNA to identify a DNA fragment (AAQ78279) containing the GAPDH promoter. A sequence (AAQ78278) encoding the GAPDH gene (gpdA) was isolated from a cDNA library. The full sequence of the genomic gpdA structural gene is given in AAQ78280 and the corresponding protein sequence in AAR65965. The GAPDH promoter is useful for expressing foreign genes
           This invention describes novel human nucleic acid (cDNA) sequences () that are highly expressed in uterine tumour tissue and which have anticancer and cytostatic activity. (A) are used (1) for recombinant expression of polypeptides (B) and (ii) to isolate complete genes. (I are used (1) to identify agents suitable for treatment of uterine or endometrial cancer; (ii) directly for treating these forms of cancer (including expression from gene therapy vectors) and (iii) for generation of specific antibodies. (A) are identified by assembling I
                                                                                                                                                                                      and
                                                                                                                                                                                                   New nucleic acid sequences expressed in uterine cancer tissues, and derived polypeptides, for treatment of uterine and endometrial canc
                                                                                                                                                                                                                                                                                                                                                                                       17-APR-1998;
                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                              Rosenthal
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DE19817948-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Endometrium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human endometrium tumour EST encoded
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A cosmid bank of T. niveum ATCC 34921 genomic DNA was screened with
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                                                                                                                                                                                                                                                                                                                           (META-) METAGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treatment;
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                                                                                                                                                                                     ived polypeptides, for treatment of uterine and
identification of therapeutic agents
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DB; AAZ42007.
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                                                                                                                                                      23; Page 307; 444pp;
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8; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             m; human;
uterine;
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 sequence tags)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein; 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumour; cancer
gene therapy;
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                                                                                                                                                                                                                                                                                              Hinzmann
from a particular tissue type before comparison
                                                                                                                                                        German
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07-APR-2000;
03-AUG-2000;
                                                                                                              sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakagawa
Tateishi
                 in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                       amino acids, nucleic acids, vitamins, saccharides and particularly L-lysine. The present sequence is a prote
                                                                                                                                                                                                                                                                                         The
                                                                                                                                                                                                                                                                                                                                                                                                       Novel polynucleotides derived from Coryneform bacteria, mutation point of a gene, measuring expression of a gene expression profile or pattern of a gene and identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               different parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular tissue. AAY59941-Y60328 repres protein fragments encoded by the human endometrium tumour cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of expression patterns. This allows a significantly longer fragment the gene to be revealed, so should reduce the number of failures associated with the fact that ESTs from different libraries may represent the control of the contr
                                                                                                                                                                                                                                                                                                                                         Claim 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-2000;
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2000JP-0159162.
2000JP-0280988.
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Senoh A,
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Ozaki A;
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14;
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                                                                                                                                                  disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y5879) can be used ir immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising
                                                                                                                                                                                                                             AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart
                                                                                                                                                                                                                                                                                                                                                                             Griffais
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-SEP-1999
                                                                                                                                                                                                                                                                                                                       Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                               Page 1086-1087; Disclosure; 1912pp; English.
                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-357842/30
                                                                                                                                                                                                                                                                                                                                                                                                                               04-NOV-1998;
21-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine;
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                         NDHLSILEAWSDNDTPY 18
ndrffklvawydnetgy 320
                                                similarity
9; Conserv
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                                                                                                                                         where the vector directs the expression C. pneumoniae.
                                                                                                                336 AA;
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97FR-0014673
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                                                            Score 46;
Pred. No.
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Pred. No.
                                                ore 46; DB
red. No. 46;
Mismatches
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Best Local
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cellulose; carbohydrate binding domain; CBD; fungi; cellulase.
           Fusarium oxysporum F-family cellobiohydrolase.
                                      AAR15238;
                                                                                                                                                                                                                                                                   Use of p53 transcription cancer diagnosis
                                                                                                                                                                                                                                                                                                                                                                                              p53 transcription tag;
neoplastic; PIG.
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                         11-FEB-1992
                                                  AAR15238 standard; Protein;
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17-SEP-1997;
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                                                                                            1 ANDHLSIL----EAWSDNDTPYLH
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                                                                                                                                       236
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97US-0059153.
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                                                                                                                                                                                                                                                      73pp; English.
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                                                                                                              37.8%;
44.0%;
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Search completed: March 27, 2002, 13:57:52 Job time: 520 sec
                                                                                                                                                                                                         Query Match 37.8%;
Best Local Similarity 24.4%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                The full-length F-family cellobiohydrolase coding sequence was isolated from a F.oxysporum cDNA library by hybridisation to PCR generated genomic oligonucleotide probes (see esp. AAQ15504). The enzyme encoded by the sequence has a CBD which is homologous to a terminal A region of T.reesei cellulase and is able to bind to insoluble (hemi)cellulosic substrates. See AAQ14838-Q14842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 12; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New fungal (hemi) cellulose degrading enzymes - for prodn. of liq. fuel gas and feed protein, have specified carbohydrate binding domain
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N-PSDB; AAQ14839.
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329 andyltvmnaclavpkcvgitvwgvsdkdswrpgdnpllyd 369
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/note= "homologous to a terminal A region of
T.reesei cellulase"
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                                                                                                                                                           -----WSDNDTPYLHD 21
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on:

March 27, 2002, 13:59:38; Search time 53.4 Seconds
(without alignments)
14.419 Million cell updates/sec

Title:
Perfect score:
119
Sequence:
119
Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched:
100059 seqs, 36664827 residues

Perfamum DB seq length: 0
Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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## SUMMARIES

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G3PC_CTYVB G3PC_TYVB G3P_CHLPN PCHA_PSEAE GAMT_HUMAN GUMF_FUSON AMP2_STRCO G3P_MELGA G3P_CHICK G3P_COLLI G3P_COLLI G3PC_MAIZE G3PC_MAIZE G3PC_RYPORVU G3P_CRYPORVU G3P_CRYPORVU G3P_CRYPORVU G3PC_RYPORVU GAMT_MOUSE TKN1_RAT GAMT_MOUSE TKN1_RAT GAMT_MOUSE TKN1_RAT GAMT_MOUSE G3PC_BOVIN	GTFB_STRMU GTFC_STRMU GTFC_STRDO GTF1_STRDO GTFS_STRDO GTFS_STRMU GJFD_STRMU GJFD_LEIME UIL16_ERV	Ib
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	45	44	43	42	41	40	39	38	37	36	35	34
	42.5	42.5	42.5	42.5	43	43	<b>4</b> 3	43	43	43	43	43
•	35.7	35.7	35.7	35.7	36.1	36.1	36.1	36.1	36.1	36.1	36.1	36.1
	764	645	491	441	2485	674	424	337	334	332	332	322
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I	YIS7_YEAST	IME2_YEAST	G6PD_ECOLI	HGD_STRCO	PTND_HUMAN	COAA_BACTJ	IVD_RAT	G3P_MYCGE	G3P2_HUMAN	G3P_RABIT	G3P_PIG	G3P_SHEEP
•	P40566 saccharomyc			Q9s2b5 streptomyce	Q12923 homo sapien	087905 bacillus th	P12007 rattus norv	P47543 mycoplasma	P04406 homo sapien	P46406 oryctolagus	P00355 sus scrofa	Q28554 ovis aries

## ALIGNMENTS

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	-!- SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES AND SOME TO A GLUCAN-BINDING PROTEIN FROM S. MUTANS.  This SWISS-PROT entry is copyright. It is produced through a collaborat between the Swiss Institute of Bioinformatics and the EMBL outstatic	1 1 1 1	Streptococcus mutans.";  FEMS Microbiol. Lett. 161:331-336(1998).  -:- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT  -:- FUNCTION: PRODUCTION OF EXPELOPMENT OF THE DENTAL  TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL  OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND ME  AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.			TT 1 GTFB_STRMU B08987; 06938 01-NOV-1988 ( 15-JUL-1999 ( 15-JUL-1999 ( GLUCOSYLTRANS GSUCOSYLTRANS GSUCOSCUS Bacteria; Firstroptoccus Streptococcus

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                                                                                                         Query Match
Best Local
                                                Matches
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InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 13.
Pfam; PF02324; Glyco_hydro_70; 1.
Pfam; PF02324; Glycosyltransferase; Sig POTENTI; 34
                                                                                                        CONFLICT
SEQUENCE
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PIR; E
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                                                          Similarity
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CATALYTIC (APPROXIMATE).
GLUCAN-BINDING (APPROXIMATE).
A REPEAT.
5 X TANDEM REPEATS.
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I -> T (IN STRAIN MT4239).
K -> R (IN STRAIN MT8148).
F -> Y (IN STRAIN MT8148).
T -> I (IN STRAIN MT8148).
A -> V (IN STRAIN MT8148).
F -> L (IN STRAIN MT8148).
F -> L (IN STRAIN MT8148).
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MT8148 )
MT8248 )
MT825 )
MT8
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POTENTIAL.
GLUCOSYLTRANSFERASE-I.
                                                        Score 119; DB 1;
Pred. No. 2.1e-10;
                                             Mismatches
                                                                                                       L (IN REF. 1).
3479B62B07694D98
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(IN STRAINS MT4239,
MT4467 AND MT8148).
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N STRAINS MT4245 A
N STRAIN MT4467).
N REF. 1).
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N STRAIN MT4251).
N STRAIN MT4239,
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MT4251).
MT8148).
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MT8148).
MT8148).
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MT4245
MT4239,
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                                                                  Length 1476;
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5 AND MT4251).
9, MT4245, MT4251
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Transferase;
SIGNAL
CHAIN
DOMAIN
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DOMAIN
DOMAIN
11

Glycosyl

hydro\_70; 1. transferase;

Signal; Repeat;

Dental

REPEAT REPEAT REPEAT REPEAT

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153022

MW;

REPEAT (INCOMPLETE).
; D4B80CBEE0AACE13 CRC64;

35 1126 1126 1126 1126 1169 1169 1227

1375 1050 1050 1375 1375 1375 1159 1200 1238

GLUCOSYLTRANSFERASE-SI.
CATALYTIC (APPROXIMATE).
GLUCAN-BINDING (APPROXIM.
2.4 A, 1 C AND 1 AC REPEAT.
A REPEAT.
A REPEAT.
C REPEAT.
AC REPEAT.

(APPROXIMATE)

1 AC REPEATS.

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RESULT 2
GTFC_STRMU
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Shiroza T., Ueda S., Kuramitsu H.K.;

Shiroza T., Ueda S., Kuramitsu H.K.;

RY "Sequence analysis of the gtfB gene from Streptococcus mutans.";

L. Bacteriol. 169:4263-4270(1887).

L. Bacteriol. 169:4263-4270(1887).

C. FUROTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT

TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE

C. OF THEIR ABILITY TO ADHERE TO SMOTH SURFACES AND MEDIATE THE

C. AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

C. -I- CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL) (N) -

C. CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL) (N) -

C. -I- SUBCELLULAR LOCATION: SECRETED.

C. -I- SUBCELLULAR LOCATION: SECRETED.

C. -I- SUBCELLULAR LOCATION: STETES WATER-INSOLUBLE GLUCANS (ALPHA

C. -I- SUBCELLULAR LOCATION SOME 1,6 LINKAGES), GTF-S SYNTHESIZES

MATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH

C. FORNS OF GLUCANS.
                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTFC_STRMU STANDARD; PRT; 1375 AA.
P13470; P05427;
01-NOV-1988 (Rel. 09, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
6LUCOSYLTRANSFERASE-SI PRECURSOR (EC 2.4.1.5) (GTF-SI)
(DEXTRANSFERASE) (SUCROSE 6-GLUCOSYLTRANSFERASE).
                                                                                                                            EMBL; M22054; AAA88592.1; -.
EMBL; M17561; AAA88599.1; -.
EMBL; M17545; JT0345
PIR; JT0345; C33135.
PIR; C33135; C33135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ueda S., Shiroza T., Kuramitsu H.K.; "Sequence analysis of the gtfC gene Gene 69:101-109(1988).
InterPro: IPR002479; CW_binding.
InterPro: IPR003318; Glyco_hydro_70.
Pfam: PF01473; CW_binding_1; 7.
Pfam: PF02324; Glyco_hydro_70; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=87308013; PubMed=3040685;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89137980; PubMed=2976010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES BINDING PROTEIN FROM S.MUTANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-349 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from Streptococcus mutans GS-5.";
                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                       rmatics and the EMBL outst
There are no restrictions
ng as its content is in
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Best Local
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                                       DOMAIN
DOMAIN
                                                                CHAIN
DOMAIN
                                                                                                               InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 16.
Pfam; PF02324; Glyco_hydro_70; 1.
                                                                                                                                                                                                                            use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GLUCOSYLTRANSFERASE-I PRECURSOR (EC 2.4.1.5)
  REPEAT
REPEAT
REPEAT
                                                                                                                                                                   HSSP;
                                                                                                                                                                           EMBL; D90213; BAA14241.1; -. PIR; A38175; A38175.
                                                                                                                                                                                                                   or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus downei (Streptococcus sobrinus)
Bacteria; Firmicutes; Bacillus/Clostridium gro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthetase).";
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Abo H., Matsumura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1317;
                                                                                           SIGNAL
                                                                                                     Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kagawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SUCROSE 6-GLUCOSYLTRANSFERASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriol, 173:989-996(1991).

Bacteriol: 173:989-996(1991).

FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N) = D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).
                                                                                                                                                                                                                                                                                                                                         D-FRUCTOSE + (1,5-ALFIN, 2-1)
DISEASE: DENTAL CARIES.
DISEASE: DENTAL CARIES.
MISCELLANEOUS: GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,3-LINKAED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES B
                                                                                                                                                                                                                                                                                                                     WATER-SCLUBLE GLUCANS (ALPHA 1,6-GLUCOSE)
FORMS OF GLUCANS.
SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES
BINDING PROTEIN FROM S.MUTANS.
                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced throueen the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANDHLSILEAWSDNDTPYLHD
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                                                                                                                                                                   P00695; 2HEE.
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   39
1093
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1158
                                                                                                                                                                                                                equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
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                                                                                                 Glyco_hydro_70; 1.
Glycosyltransferase; Signal;
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1592
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T., Kodama T.,
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95.2%;
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GLUCOSYLTRANSFERASE-I.
CAPLATTIC (APPROXIMATE).
GLUCAN-BINDING (APPROXIMATE).
6.5 X TANDEM REPEATS.
1.
2.
3.
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                                                                                         POTENTIAL
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                                                                                                                                                                                                                                                                                            is produced through
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                                                                                                    Repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     group;
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                                                                                                     Dental caries
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                                                                                                                                                                                                                                                                             EMBL outstation
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                                                                                                                                                                                                                                                                                a collaboration
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Best Local S
Matches 18
          Transferase; Glycosyltransferase; S SIGNAL 1 38 POTENT CHAIN 39 1597 GLUCOSY DOMAIN 1099 1597 GLUCAN-DOMAIN 1099 1597 1.25 A.
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sobrinus MFe28.";
J. Bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1989 (Rel. 11, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GLUCOSYLTRANSFERASE-I PRECURSOR (EC 2.4.1.5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last seg
15-DEC-1998 (Rel. 37, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRDO
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REPEAT
                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                            InterPro; IPR002479; GW_binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 19.
Pfam; PF02324; Glyco_hydro_70; 1.
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                                                                                                                                                                                                                             EMBL; M17391; AAC63063.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLANGOUS: GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA MISCELLANGOUS: GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES BOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N)
D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).
SUBCELLULAR LOCATION: SECRETED.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES BINDING PROTEIN FROM S.MUTANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND ME AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.
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; Bacillus/Clostridium group;
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Pred. No. 1.
                                                        GLUCOSYLTRANSFERASE-I.
CATALYTIC (APPROXIMATE)
                 GLUCAN-BINDING (APPROXIMATE)
1.25 A, 2 B, AND 5 AC REPEAT
                                                                                                    POTENTIAL.
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REPEAT
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BCOA66D079351ECF CRC64;
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.1e-08;
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                                                                                                                        Repeat;
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                                                                                                                        Dental caries.
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                   REPEATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DEXTRANSUCRASE)
                                                                                                                                                                                                                                                                                                                                                       restrictions
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P29336;
01-DEC-1992 (Rel. 2
01-DEC-1992 (Rel. 2
01-APR-1993 (Rel. 2
                                                                                                                                                                                                                                                                                                                                                                           Gilmore K.S., Russell R.R., Ferretti J.J.;
"Analysis of the Streptococcus downei gtfS gene, which specifies glucosyltransferase that synthesizes soluble glucans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
GLUCOSYLTRANSFERASE-S PRECURSOR (EC 2.4.1.5)
(SUCROSE 6-GLUCOSYLTRANSFERASE).
                                PIR; A41483; A41483.
InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 10.
Pfam; PF02324; Glyco_hydro_70; 1.
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                                                                                                                  entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                         Infect.
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus
              SIGNAL
                         Transferase;
                                                                                             EMBL; M30943; AAA26898.1;
                                                                                                                                           modified
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                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90316665; PubMed=2142479;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1317;
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                                                                                                                                                                                                                                                                     GCT. Immun. 58:2452-2458(1990).

FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N) = D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).

ENZYME REGULATION: GLUCAN SYNTHESIS BY GTF-S IS INDEPENDENT OF PRIMER GLUCAN UNLIKE GTF-I.
                                                                                                                                                                                                                         1,6-GLUCOSE).
SIMILARITY: TO OTHER
                                                                                                                                                                                                                                               MISCELLANEOUS: GTF-S
                                                                                                                                                                                                                BINDING PROTEIN FROM
                                                                                                                                                                                                                                                             DISEASE: DENTAL CARIES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                          non-profit institutions as long and this statement is not removed.
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Glycosyltransferase; Signal; Repeat; Dental caries 1 36 OR 37 (POTENTIAL). 37 1365 GLUCOSYLTRANSFERASE-S.
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; Bacillus/Clostridium group; Streptococcaceae;
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                                                                                                                                                                                                              GLUCOSYLTRANSFERASES S.MUTANS.
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Pred.
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B REPEAT.
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REPEAT (INCOMPLETE)
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No. 1.2e-08;
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                                                                                                                                                                                                                                                  WATER-SOLUBLE
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                                                                                                                                          Usage
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Best Local :
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01-FEB-1996 (Rel. 33, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GLUCOSYLTRANSFERASE-S PRECURSOR (EC 2.4.1.5)
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Honda O., Kato C., Kuramitsu H.K.;
"Nucleotide sequence of the Streptococcus
the glucosyltransferase-S enzyme.";
J. Gen. Microbiol. 136:2099-2105(1990).
                                                                                                                                                                                                                                                                                                              STRAIN=MT4239, MT4245, MT4251, MT4467, MEDLINE=98231643; PubMed=9570124; Fujlwara T., Terao Y., Hoshino T., Kawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTFD.
Streptococcus mutans
                                                                      This
                                                                                                                                                                                                                                                                Streptococcus mutans."; FEMS Microbiol. Lett. 161:331-336(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
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                                                                                                                                        FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTIAL PLAQUE BECAUSE OF THEIR ABILITY TO ADHERE TO SMOOTH SUFFACES AND MEDIATE THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N) = D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).

SUBCELLULAR LOCATION: SECRETED.

DISEASE: DENTIAL CARLES.

MISCELLANEOUS: GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA I.3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES
                                                                                          FORMS OF GLUCANS.
SIMILARITY: TO OTHER
BINDING PROTEIN FROM
                                                                                                                                WATER-SOLUBLE GLUCANS
                                                                     SWISS-PROT entry is copyright.
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                                                                                           GLUCOSYLTRANSFERASES AND S.MUTANS.
                                                                                                                             SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA ND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES BOTH (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH
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GLUCAN-BINDING (APPROXIMATE).
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Matches 15
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EMBL; D88655; BAAA26103.1; -.
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EMBL; D88659; BAA26111.1; -.
EMBL; D88659; BAA26111.1; -.
EMBL; D88669; BAA26115.1; -.
EMBL; D88669; BAA26115.1; -.
EMBL; D89979; BAA26121.1; -.
EMBL; D89079; BAA26121.1; -.
EMBL; D89079; BAA26121.1; -.
EMBL; D89079; BAA26121.1; -.
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AND MT8148).

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MT4245 AND
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UL16_EBV

P03221;

21-JUL-1986 (Re

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BGLF2 PROTEIN.
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Q01558;
O1-APR-1993 (Rel. 25, Created)
O1-FEB-1994 (Rel. 28, Last sequence update)
O1-JUL-1999 (Rel. 38, Last annotation update)
GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC (EC 1.2.1.12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X65220; CAA46323.1;
PIR; S25142; S25142.
PIR; B48445; B48445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-SSP. MEXICANA;
MEDLINE-93063042; PubMed-1435864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leishmania mexicana.
Eukaryota; Euglenozoa;
NCBI_TaxID=5665;
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-!- SUBUNIT: HOMOTETRAMER.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphate dehydrogenase in Leishmania mexicana
Mol. Biochem. Parasitol. 55:115-126(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00071; GAPDH;
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InterPro; IPR000173;
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s; PR00078; G3PDHDRGNASE.
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00xidoreductase; NAD.
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175 ACTIVATES THIOL GROUP DURIN
175 175 ACTIVATES THIOL GROUP DURIN
175 175 ED4B6D8E8A207F1E CRC64;
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Pred. No. 0.15
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Matches 7
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EMBL; V01555; CAA24831.1; -
EMBL; S77132; AAB21113.1; -
PIR; A03784; QQBE40.
PIR; S33036; S33036.
                                        STRAIN=427;
MEDLINE=91249838; PubMed=2040303;
Michels P.A.M., Marchand M., Kohl L., Allo
Opperdoes F.R.;
"The cytosolic and glycosomal isoenzymes
"The cytosolic and glycosomal brucei have
                                                                                                                                                                                                                                             01-MAR-1989
01-MAY-1992
15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transcripts from the BamHI G region of the Epstein-Barr virus and expression of BLET2.";
J. Gen. Virol. 72:3047-3055(1991)
-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1
HSV-6 ORF11R, EHV-1 46, HCMV UL94, EBV BDLF2, AND VZV 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-84270667; PubMed-6087149; Baser R., Bankler A.T., Biggin M.D., Gibson T.J., Hatfull G., Hudson G.S. Tuffnell P.S., Barrell B.G.; "DNA sequence and expression of the Nature 310:207-211(1984).
                             dehydrogenase in Trypanosoma brucei
relationship.";
                                                                                                                                                                                   Trypanosoma brucei brucei.
Eukaryota; Euglenozoa; Kir
                                                                                                                                                                                                                               GLYCERALDEHYDE
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P10097;
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Chen M.R., Hsu T.Y., Lin S.W., Chen J.Y., Yang C.S.;
"Cloning and characterization of cDNA clones corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-92113548;
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                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                   NCBI_TaxID=5702;
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                  GAPDH)
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               Biochem. 198:421-428(1991)
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nilarity 41.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      336 AA;
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(Rel. 22, Last sequence update)
(Rel. 38, Last annotation update)
(Rel. 38 -PHOSPHATE DEHYDROGENASE, CYTOSOLIC (EC
                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=6087149;
A.T., Biggin M.D., Deininger P.
ull G., Hudson G.S., Satchwell
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Pred. No. 2
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2.7;
                                            of glyceraldehyde-3-phosphate a distant evolutionary
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01-OCT-1996 (Rel. :
01-OCT-1996 (Rel. :
01-NOV-1997 (Rel. :
14YPOTHETICAL 31.8 HYPOTHETICAL 31.8 F
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CONFLICT
SEQUENCE
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"Glyceraldehyde-phosphate dehydrogenase from Trypanosoma brucei.
Comparison of the glycosomal and cytosolic isoenzymes.";
Eur. J. Biochem. 162:501-507(1987)
Eur. J. Biochem. 162:501-507(1987)
- i- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE
                        van Dyck L., Tettelin H., Purnelle B., "An 18.3 kb DNA fragment from yeast chunknown open reading frames, the gene i of Ty and three tRNA genes.";
Yeast 13:171-176(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INIT_MET BINDING
                                                                                        SEQUENCE FROM N.A.
STRAIN=S288C / FY1679;
MEDLINE=97197982; PubMed=9046098;
                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomyc
Saccharomycetales; Saccharomycetaceae; Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
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-- SUBCELLULAR LOCATION: CYTOPLASMIC.
-- SUBCELLULAR LOCATION: CYTOPLASMIC.
 This SWISS-PROT entry is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00078; G3PDHDRGNASE. PROSITE; PS00071; GAPDH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000173; Pfam; PF00044; gpdh;
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MEDLINE=87161817; PubMed=3830153;
                                                                                                                                            NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT
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34, Last sequence update)
35, Last annotation update
KDA PROTEIN IN NUP57-MEP1
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149
176
72
56
60
60
35503
                                                                                                                                                         Ascomycota; Saccharomycotina;
Saccharomycetaceae; Saccharom
                                                                                                                                                                                                                                                                                                                                                                                                    39.9%;
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copyright.
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ACTIVATES THIOL GROUP DURIL
R -> I.
A -> T (IN REF. 2).
A -> T (IN REF. 2).
O -> K (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                        323
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Pred. No. 4
                                                                                                                                                                                                                                                                           PRT;
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-> K (IN REF. 2).
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                                                B., Goffeau A.;
chromosome VII carries
ne for an Asn synthase,
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                                                                                                                                                                                                                     update)
 is
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SE OF
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                                                                                                                                                                    Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                Length 330
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 through a collaboration
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EMBL outstation

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G3P_CHLPN
ID G3P_C
GAP C
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                                                                    Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314 (2000).

Nucleic Acids Res. 28:2311-2314 (2000).

-i- CATALYTIC ACTYUTY D. D-GLYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE + NADH.

-i- PATHWAY: FIRST STEP IN THE SECOND PHASE OF GLYCOLYSIS.

-i- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).

-i- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).

-i- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).

-i- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
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Q9Z7T0; Q9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC 1.:
GAP OR GAPA OR CPN0524 OR CP0123.
Chlamyddia pneumoniae (Chlamydophila pneumoniae)
Bacteria; Chlamyddiales; Chlamyddiaceae; Chlamydop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg White O., Hickey E.K., Peterson J., Utterback T., Berry Linher K., Weidman J., Khouri H., Craven B., Bowman C., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Eisen J., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE...
STRAIN-CWL029;
MEDLINE-9206606; PubMed=10192388;
MEDLINE-9206606; PubMed=10192388;
Marathe R., Lammel C., F.
Davis R.W., Stephens R.
---isa and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20330349; PubMed=10871362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20150255; PubMed=10684935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-AR39
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the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequences of Chlamydia trachomatis pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=83558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olinger L., Grimwood J., Davis R.W., "Comparative genomes of Chlamydia pno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217
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                                                         DEHYDROGENASE FAMILY.
SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILESCADSNSPYIH
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Z72905; CAA97130.1;
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  produced through a collaboration
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Dodson R.,
Salzberg S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J.F.,
K., Bas
Dodson
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RESULY 12
PCHA_PSEAE
ID PCHA_P
AC 051508
DT 01-NOV
DT 20-AUG
DE SALICY
GN PSEUdo
OC PSEUdo
OC PSEUdo
OX NCBI_T
RN [1]
RP SEQUEN
RC STRAIN
RX MEDLIN
RA Serinc
RI PSEUGO
RF PSEUG
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Matches 9
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the Euro
use by
                                                                                                                                                                                                      SEQUENCE FROM N.A.

STRAIN-ATCC 15692 / PAO1;

MEDLINE=20437337; PubMed=10984043;

MEDLINE=20437337; PubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Smith K.A., Spencer D.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serino L., Reimmann C., Baur H., Beyeler M., V "Structural genes for salicylate biosynthesis Pseudomonas aeruginosa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
SALICYLATE BIOSYNTHESIS ISOCHORISMATE
                                                                                                                                        "Complete genome sequence of Pseudomonas aeruginosa opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-96086939; PubMed-7500944;
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Q51508;
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Pfam; PF00044; gpdh; 1.
PRINTS; PRO0078; G3PPHDRGNASE.
PROSITE; PS00071; GAPDH; 1.
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EMBL; AP002547; BAA98831.1;
HSSP; P06977; IGAE.
TIGR; CP0123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCHA OR PA4231.
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                       CATALYTIC ACTIVITY:
PATHWAY: SALICYLATE
SIMILARITY: STRONG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                     FUNCTION:
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9; Conserv
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                                                                                                                     INVOLVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                          249:217-228(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151
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                                                                                                                  ΙN
                                                                     CHORISMATE - ISOCHORISMATE
                            Ö
                                                  BIOSYNTHESIS
                                                                                                                  THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gamma subdivision;
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                            OTHER
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Pred.
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                                                                                                                     CONVERSION
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                          ISOCHORISMATE SYNTHASES;
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No.
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SYNTHASE
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7.7;
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                                                                                                                  CHORISMATE
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s from
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6).
                          WEAK,
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RESULT 13
GAMT_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GUANIDINOACETATE N-METHYLTRANSFERASE (EC 2.1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q14353;
Kronmiller B., Arellano A., Montgomery M., Ow D., Kobayashi A., Olsen A.S., Carrano A.V.; Kobayashi A. (Jub-198) to the EMBL/GenBank/DDBJ data - I - CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE +
                                                             SEQUENCE FROM N.A.

Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W

Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Sti

Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Garnes

Phan H., Velasco N., Do L., Regala W., Terry A., Garnes

Danganan L., Poundstone P., Christensen M., Georgescu A.

Liu S., Attix C., Andreise T., Trankheim M., Amico-Kelle

Coeffeld J., Duarte S., Lucas S., Bruce R., Thomas P., Q
                                                                                                                                                                                                                                                                                          syntenic region on 19p13.3, homologous to band C 10, but GAMT is not mutated in jittery mice."; Biochem. Biophys. Res. Commun. 238:723-727(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                              methyltransferase cDNA.";
Biochim. Biophys. Acta 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAMT
                                                                                                                                                                                                     Isbrandt D., Schmidt A.; "Gene structure of human submitted (SEP-1999) to
                                                                                                                                                                                                                                                                                                                                             "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isomerase;
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning and sequence analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96138544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                             Jenne
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97472276;
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human guanidinoacetate methyltransferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Conserv
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476 AA; 52071 MW; D0F6AFD9CDCF9CF5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                PubMed=9325156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=8547310;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Acta 1264:265-267(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                         n guanidinoacetate N-methyltransferase."; the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of human guanidinoacetate N-
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                                                                                    Amico-Keller G.,
               databases
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                                                    Nolan
   GUANIDOACETATE
                                                                    P., Quan G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
                                                                                                                                                       A.W.
                                                                                                                                                                                                                                                                                                                               mouse chromosome
                                                                                                                                       Stilwagen
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RESULT 14
GUNF_FUSOX
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Query Match
Best Local S
Matches 11
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EMBL; AF010246; AAD04781.1; J
EMBL; AF010247; AAD04781.1; J
EMBL; AF010247; AAD0461.1; -
EMBL; AG005329; AAC27668.1; -
MIM; 601240; -
                                                                                                                                                                                           Hagen F.S., Opshall A., McKnight G.L., O'Hara P.J.;
"The use of conserved cellulase family-specific sequences cellulase homologue cDNAs from Fusarium oxysporum.";
Gene 150:163-167(1994).
-I- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-GLUCO:
LINKAGES IN CELLULOSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PUTATIVE ENDOGLUCANASE TYPE F PRECURSOR (EC 3
GLUCANASE) (CELLULASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P46239;
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GUNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transferase; Methyltransferase SEQUENCE 236 AA; 26318 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z49878; CAA90035.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota;
Hypocreales; mitosporic Hypocr
NCBI_TaxID=5507;
                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-95047531; PubMed-7959045;
Sheppard P.O., Grant F.J., Oort P
                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                     Fusarium oxysporum.
                                                                        modified and
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PATHWAY: LAST STEP OF CREATINE BIOSYNTHESIS.

DISEASE: DEFECTS IN GAMT ARE BIOSYNTHESIS FOR NEUROLOGIC SYNDROME AND MUSCULAR HYPOTONIA. BIOCHEMICALLY IT IS CHARACTERIZED BY LOW EXCRETION OF CREATINE, DEFICIENCY OF CREATINE AND CREATINE PHOSPHATE, AND SIMULTANEOUS ACCUMULATION OF GUANIDINOACETATE IN
                                                                                                                                                                             SIMILARITY: CONTAINS SIMILARITY: BELONGS T
                                                                                                                                                               HYDROLASES)
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                                                                     this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.8%;
                                                                                                                                                                             S 1 FUNGAL-TYPE CELLULOSE-BINDING TO CELLULASE FAMILY F (FAMILY 10
                                                                                                                                                                                                                                                                                                                                                                         Hypocreales;
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                                                                                                                                                                                                                                                                                                                                                                                         Pezizomycotina;
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No.
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                                                                                                                                                                                                                           OF 1,4-BETA-D-GLUCOSIDIC
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7.3;
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d the EMBL outstation -
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EMBL;

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RESULT
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st Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O60394;
O60394;
O1-NOV-1997 (Rel. 35, Created)
O1-NOV-1997 (Rel. 35, Last sequence update)
O1-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
XAA-PRO AMINOPEPTIDASE II (EC 3.4.11.9) (X-PRO AMINOPEPTIDASE II)
XAA-PRO AMINOPEPTIDASE P II) (APP) (PEPP II) (AMINOACYLPROLINE AMINOPEPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00734; CBD_1; 1.
Pfam; PF00331; Glyco_hydro_10; 1.
Pfam; PF00334; GLHYDRLASE10.
PRINTS; PR00134; GLHYDRLASE11.
ProDom; PD001821; CBD_fungal; 1.
SMART; SM00236; fCBD; 1.
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ACT_SITE
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SEQUENCE
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                                                                                                                                                                               -:- CATALTRIC ACTIVITY: RELEASE OF ANY N-TERMINAL AMINO ACID,
INCLUDING PROLINE, THAT IS LINKED WITH PROLINE, EVEN FROM A
DIPEPTIDE OR TRIPEPTIDE.
-:- COPACTOR: ZINC OR MANGANESE.
-:- SUBUNIT: HOMODIMER (BY SIMILARITY).
-:- WISCELLANEOUS: IN STREPTOMYCES LIVIDANS, THERE ARE TWO GENES
(PEPPI AND PEPP2) WHICH ENCODE AMINOPEPTIDASE P.
-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M24B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES-S.lividans; STRAIN-66;
MEDLINE-94176084; PubMed-7765336;
Butler M.J., Aphale J.S., Dizonno M.A., Krygsman P., Walczyk E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
DOMAIN
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Oliver K., Harris D.,
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InterPro; IPR001000; Glyco_hydro_10.
                                                                                                                                                                                                                                                                                                                                                                                                      "Intracellular aminopeptidases in Streptomyces lividans 66.";
J. Ind. Microbiol. 13:24-29(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rajandream M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinomycetales;
NCBI_TaxID=1902,
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PROSITE; PS00591; GLYCOSYL_HYDROL_F10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Malek L.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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license agreement (See http://www.isb-sib.ch/announce/
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Bentley S.D.,
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CATALYTIC.
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NUCLEOPHILE (BY SIMILARITY).
B3C3807C07D3C0EC CRC64;
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InterPro; IPR001994; Peptidase_M24.
InterPro; IPR00131; Pro_dipeptdse.
Pfam; PF00557; Peptidase_M24; I.
PROSITE; PS00491; PROLINE_PEPTIDASE;
Hydrolase; Manlonpeptidase; Manganese;
SEQUENCE 470 AA; 51924 MW; 0D3D33
                                                                                                                                                                                                                                                                      EMBL; AL359949; CAB95809.1; EMBL; L23174; AAB00325.1; -.
                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                               262
                                                                                      1 ANDHLSILEAWSDNDTP
                                                              AGEHATIMH-WTDNDGP
                                                                                                                 Similarity
8; Conserva
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470 AA; 51924 MW; 0D3D33CE256523C2 CRC64;
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	44	44.5	44.5	45	45	45	45	45.5	46	46	47	47	47	47	47.5	47.5	47.5	48	49	49.5	50	51	52	57	58	60
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## ALIGNMENTS

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FEMS Microbiol. Lett. 161:331-336(1998).
EMBL; D88661; BAAZ6114.1;
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InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 9.
Pfam; PF02324; Glyco_hydro_70; 1.
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SEQUENCE :
                                                                                                                                                          MEDLINE=98231643; PubMed=9570124; Fujiwara T., Terao Y., Hoshino T.,
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Fujlwara T., Terao Y., Hoshino T., Kawabata
Kimura S., Hamada S.;
"Molecular analyses of glucosyltransferase
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       MEDLINE-98231643; PubMed-9570124;
Fujiwara T., Terao Y., Hoshino T., Kawabata S., Kimura S., Hamada S.;
"Molecular analyses of glucosyltransferase ge "Molecular analyses of glucosyltransferase ge Streptococcus mutans.";
FEMS Microbiol. Lett. 161:331-336(1998).
EMBL; D89978; BAAZ6120.1;
Interpro; IPR002479; CW_binding.
Interpro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 9.
Pfam; PF02324; Glyco_hydro_70; 1.
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01-JUN-2001
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01-AUG-1998
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EMBL; D88658; BAAZ6110.1; .
InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 10.
Pfam; PF02324; Glyco_hydro_70; 1.
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01-AUG-1998 (TrembLrel.
01-JUN-2001 (TrembLrel.
GLUCOSYLTRANSFERASE-SI.
  Transferase.
                                                                                                                      SEQUENCE FROM N.A. STRAIN=MT4467;
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"Molecular analyses of glucosyltransferase
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
GLUCOSYLTRANSFERASE-I PRECURSOR (EC
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01-JAN-1998 (Tremblrel. 05
01-JUN-2001 (Tremblrel. 17
GLUCOSYLTRANSFERASE GTF-I.
Bacteria; Firmicutes;
Streptococcus.
NCBI_TaxID=1310;
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Q55263;
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NCBI_TaxID=1310;
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Transferase.
1590 AA;
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EMBL; D63570; BAA09792.1; -.
InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 15.
Pfam; PF02324; Glyco_hydro_70; 1.
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Bacteria; Firmicutes; I
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85.7%;
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95.2%;
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RSOR (EC 2.4.1.5) (DEXTRANSUCRASE) (SUCROSE
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Pred. No. 2e-0
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01-NOV-1999
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Bacteria; Fi
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01-JUN-2001
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                                NCBI_TaxID=1245;
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SO FTT DR
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"S.cricetus glucosyltransferase(gtfS and gtfT) ge
submitted (MAR-1999) to the EMBL/GenBank/DDBJ dat
EMBL; ABB08123; BAA77236.1; -.
HSSP; P06278; IVJS.
InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
pfam; PF01473; CW_binding_1; 10.
pfam; PF012324; Glyco_hydro_70; 1.
plasmid.
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Pfam; PF01473; CW_binding_1; 16.

Pfam; PF02324; Glyco_hydro_70; 1.

Signal; Transferase; Glycosyltransferase.

SIGNAL 1 38 POTENTIAL.

CHAIN 39 1590 GLUCOSYLTRANSFERASE-I.

SEQUENCE 1590 AA; 175955 MW; C3C83A57CF3C2B0E C
                                                                                                                           Q9LCJ7;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2001 (TrEMBLrel. 17,
SEQUENCE FROM N.A. STRAIN-NRRL B-512F;
                                                                     Leuconostoc mesenteroides
Bacteria; Firmicutes; Bac
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71.4%;
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Pred. No. 4.5e-08;
3; Mismatches 0
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                                                                      Lactobacillaceae;
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MEDLINE-20169623;

PubMed=10705445;

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RESULT
Q9L466
RESULT 11
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Q9L466;
01-OCT-2000 (TremBLrel. 15, C
01-OCT-2000 (TremBLrel. 15, I
01-JUN-2001 (TremBLrel. 17, I
DEXTRANSUCRASE (EC 2.4.1.5).
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-NRRL B-1355;
Arguello-Morales M.A., Remaud-Simeon M., Pizzut S., Sarci
Millemot R.M., Monsan P.;
"Sequence analysis of the gene encoding alternansucrase,
"Sequence analysis of Leuconostoc mesenteroides NRRL
                                                                                                                            052224
052224;
                                                                                                                                                                                                                                                                                                                        glucosyltransferase from Leuconostoc mesentero Submitted (CCT-1999) to the EMBL/GenBank/DDBJ EMBL; AJ250172; CAB76565.1; -
InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 14.
Pfam; PF01473; CW_binding_1; 14.
Pfam; PF02324; Glyco_hydro_70; 1.
Transferase; Glycosyltransferase.
SEQUENCE 1477 AA; 164886 MW; E6F5710DEDFCB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Funane K., Mizuno K., Takahara H., Kobayashi "Gene encoding a dextransucrase-like protein mesenteroldes NRRL B-512F.";
Biosci. Biotechnol. Biochem. 64:29-38(2000). EMBL; AB020020; BAA90527.1; -. InterPro; IPR003318; Glyco_hydro_70. Pfam; pF02324; Glyco_hydro_70; 1. SEQUENCE 1016 AA; 110343 MW; 8896EFDE13CC
                                                                        01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-JUN-2001 (TrEMBLrel. 17, GLUCOSYLTRANSFERASE (EC 2.4
                        Bacteria; Firmicutes;
                                                  DSRB.
                                                               GLUCOSYLTRANSFERASE)
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                                     Leuconostoc mesenteroides
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548 SNQHVSILEDWSDNDAEYVKD 568
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66.7%;
                        Bacillus/Clostridium
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No.
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0.0079;
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                      group; Lactobacillaceae;
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RESULT
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Best Local Similarity 66.
Matches 14; Conservative
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Best Local Similarity 66.7
Matches 14; Conservative
                                                   Q9LCH3
Q9LCH3;
Q1-OCT-2000
01-OCT-2000
01-JUN-2001
                                                                                                                                                                                                                                                          Kim H.-S., Kim D., Ryu H.-J., Robyt J.F.;
"Leuconostoc mensenteroides B-742CB, a dextransucrase gene.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF294469; AAG38021.1;
InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01273; CW_binding_1; 14.
Pfam; PF02324; Glyco_hydro_70; 1.
SEQUENCE 1508 AA; 168542 MW; E2FCFA0F87AE4F3A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monchois V., Remaud-Simeon M., Monsan P., Willemot R.M.;
FEMS Microbiol. Lett. 0:0-0(1998).
-i-CATALYTIC ACTIVITY: SUGROSE + ((1.6)-ALPHA-D-GLUCOSYL)(N) -
FRUCTOSE + ((1.6)-ALPHA-D-GLUCOSYL)(N+1).
EMBL; AF030129; AAB95453.1; -
InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01373; CW_binding_1; 14.
Pfam; PF01373; CW_binding_1; 14.
Pfam; PF02324; Glyco_hydro_70; 1.
Transferase; Glycosyltransferase.
SEQUENCE 1508 AA; 168511 MW; E70CECB57A70D1F0 CRC64;
        Streptococcus oralis.
Bacteria; Firmicutes;
                                 GTFR.
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SEQUENCE FROM N.A.
STRAIN-NRRL B-1299;
                                           GLUCOSYLTRANSFERASE
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Bacteria; Firmicutes; Bacillus/Clostridium
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         Bacillus/Clostridium
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Pred. No.
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.0081;
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          Streptococcaceae;
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN-ATCC10557;

MEDLINE-20231779; PubMed-10768934;

Fujiwara T., Hoshino T., Ooshima T., Sobue S., Hamada S.;

"Purification, characterization, and molecular analysis o-

"nocoding glucosyltransferase from Streptococcus oralis.";

Infect. Immun. 68:2475-2483(2000).

EMBL; AB025228; BAA95201.1; -...
                                                                                                                                                                                                              Sulavik M.C., Tardif G., Clewell D.B.;
"Identification of a gene, rgg, which regulates expression of
glucosyltransferase and influences the Spp phenotype of Strepgordonii Challis.";
                                                                                                                                  InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70
Pfam; PF01473; CW_binding_1; 18.
                                                                                                                                                                                                                                                                                                                                      Vickerman M.M., Sulavik M.C., Clewell D.B.; "Molecular analysis of Streptococcus gordonii glucosyltransferase
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MEDLINE=96157084; PubMed=8586195;
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InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 17.
Pfam; PF02324; Glyco_hydro_70; 1.
                                                                                                               Transferase.
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[2]
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HLSILEAWSDNDTPYLHD
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Last sequence update)
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Pred. No.
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Pred. No. 0.012;
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                                    Mismatches
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0.012;
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Job time:

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RESULT
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AC Q9
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DT 01
DT 01
DT 01
DT 02
OC 01
DT 02
CO 02
CO 02
CO 03
CO 04
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Best Local Similarity 66.7
Matches 14; Conservative
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Q9ZAR4;
01-MAY-1999
01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning and Molecular Characterization of Dextransucrase Leuconostoc mesenteroides NRRL B-512F.";
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U81374; AADI0952.1; ...
InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 16.
Pfam; PF01473; CW_binding_1; 16.
Pfam; PF01324; Glyco_hydro_70; 1.
SEQUENCE 1527 AA; 169709 MW; 1DFAFA237C743398 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-NRRL B-512-F;
Bhatnagar R., Singh D.K.S.;
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Bacteria; Firmicutes; Bacillus/Clostridium
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd
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L. mesenteroides a
Alpha-D-glucosyltr
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AAG23447	AAM36026	AAY20666	AAR84561	AAB94409	AAB18886	AAB18887	AAY17246	AAB94596	AAR84562	AAB97070	AAG70686	AAG90051	AAY25684	AAG82330	AAE01115	AAM40493	AAM40492 .	AAM38706	AAE07045	AAE06775	AAE04835	AAB85363	AAW87890	AAR07464	AAY06263	AAE06776	AAE06786	AAB40856	AAY19779	AAY58277	AAY19780	48	AAG92736
- 73	de #1006	Human neurofilamen		Human protein sequ	A human prolactin	$\vdash$		Human protein sequ		Human polypeptide	S cerevisiae apopt	C glutamicum prote	a	S. epidermidis ope	Human gene 2 encod	Human polypeptide	Human polypeptide	Human polypeptide			Human SGP001 phosp	Human phosphatase	Protein encoded by	eptide with		speci	speci	man ORFX ORF	B. burgdorferi ant	liothis armic	ri an	uman SGP006 pho	C glutamicum prote

## ALIGNMENTS

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                                                                                                                                                             DNA sequence glucosyl:transferase-I - comprises Streptococcus sobrinus DNA sequence with at least one nucleotide added or
                                                                                                                                                                                                                                                                                           WPI; 1993-079449/10:
N-PSDB; AAQ37760.
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                                                                                                                                                                                                                                                                                                                                                                                                                         (FUKU/) FUKUI I.
(KATO/) KATO K.
                                    Page
                                    15;
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Best Local S
Matches 16
                         fructose is then isolated from the medium. Cosmetic products or foodstuffs containing alternan can be produced. Recombinant production alternan sucrase is advantageous as it provides a cost effective means producing fructose for high fructose containing syrups, production of which previously has been achieved by costly production from maize starch. This sequence represents the Leuconoston mesanternian alternation.
                                                                                                                                                                                                             gene is useful for the fermentative production of alternan (a carbohydrate) and/or fructose by secreting the enzyme into a saccharose-containing culture medium. Alternatively, the enzyme is contacted with a saccharose-containing solution. The alternan and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim la; Page
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   sucrase
                                                                                                                                                                                                                                                                                                                                          alternan sucrase (E.C. 2.4.1.140 - an enzyme, that belongs to glucosyltransferase group) The recombinant, purified alternan
                                                                                                                                                                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     production
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    mesenteroides alternan sucrase protein

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This sequence represents the Leuconostoc mesenteroides alternan protein which is described in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Welsh T,
                                                                                                                                                                                                                                                                                                                                                                              describes a novel nucleic acid molecule (I) se (E.C. 2.4.1.140 - an enzyme, that belongs
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FOERDERUNG WISSENSCHAFTEN
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Query Match
Best Local Similarity
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                                                                                                                              The sequence represents an alpha-D-glucosyltransferase from Streptococcus salivarius. The enzyme is primer independent, and produces soluble glucan from sucrose. A gene encoding the enzyme may be cloned and expressed in Escherichia coli using a subclone of phage lambda-Cl3, e.g. plasmid pGSG501 or plasmid pGSG502. The DNA may also be expressed in a transgenic plant, to improve the level of stored carbohydrate in a pasture plant which normally contains low levels, or to prevent degradation of stored carbohydrate during plant senescence. Dextran may be isolated from the plant, for use as a food binder or pharmaceutical additive. Primer independence ensures that the enzyme will be functional in plants. The glucan is poorly degraded in plants but easily degraded by bacteria in the rumer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alpha-D-glucosyltransferase; primer independent; soluble gl
sucrose; transgenic plant; cloning; Escherichia coll;
phage lambda-Cl3; vector; plasmid pcSc501; plasmid pcSc502;
gene transfer; crop improvement; storage carbohydrate; past
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 16-20; 31pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plants contg. new bacterial DNA encoding glucosyl transferase activity - retain higher levels of stored carbohydrate(s) in
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N-PSDB; AAT13139.
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(JACQ/) JACQUES N
(SIMP/) SIMPSON C
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                                                                                                                                              The present sequence represents a Haemophilus influenzae adhesin (Hia) Crost protein from the non-typeable Haemophilus influenzae (NTH1) strain 12. His genes and proteins have antiinflammatory, auditory and antibacterial activities, and can be used in the production of a vaccine. An immunogenic composition comprising an Hia gene, a polypeptide encoded by an Hia gene, or a recombinant Hia polypeptide is useful for inducing protection against disease caused by Haemophilus strains in a susceptible host, preferably a human. An Hia protein is useful as an artigen, in immunogenic preparations including vaccines, as a carrier for other immunogenic preparations including vaccines, as a carrier is useful for treating diseases caused by the infection of Haemophilus Crompared to the low recovery of native protein from Haemophilus compared to the low recovery of native protein from Haemophilus confluenzae species. A truncated protein has a significantly higher amount of recovery than a full-length protein.
                                                     Query Match
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Matches 7
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antibacterial; meningitis; epiglottitis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CONN-) CONNAUGHT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  661
42
                                                    Local Similarity nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYSFIRAHDSEVQDLIA 19
:| |:||||||| ::|
nyifvrahdsevqavla 677
             PSYSFIRAHDSEVQDLIA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-618897/59.
                                                                                                                                                                                                                                                                                                                                                                                                                                antigens
ion :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SM,
                                                                                                                                                                                                                                                                                                                                                                                                Fig 25; 275pp;
                                                                                                                          616 AA;
                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus influenzae adhesin; NTHi; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0268347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                  44.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klein
59
                                                                                                                                                                                                                                                                                                                                                                                                English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antigen
                                                     6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             616
                                                                  Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MH.
                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiinflammatory;
                                                                  DВ
32;
                                                                                21;
                                                    5.
                                                                              Length 616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               otitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             auditory;
                                                                                                                                                                                                                                                                                                                                                                                                                                           n protein, for influenzae
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                                                    Gaps
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AAW61347
ID AAW6
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AC AAW6
AC AAW6
AX 12-(
AX 12-(
AX TRI)
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                                                                                                                                      RESULT
                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-FEB-1997;
21-AUG-1996;
31-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                             Telomerase protein of higher animals and humans and gene encoding it - for use in diagnosis of cancer, screening of telomerase inhibitors and elucidation of biological control mechanisms
                                                                                                                                                                                                                                                                                                               inhibitors can be screened by measuring their effect on the assay of the active form in cells or tissues. The polypeptide and DNA coding for it can be used in the elucidation of biological control
                                                                                                                                                                                                                                                                                                                                               The present sequence represents a human protein component of telegraph or RNA encoding the telomerase protein component or its fragments can be used as a nucleotide probe for the detection of cancer cells and for diagnosis of cancer. Potential telomerase
            ageing;
                      TRIP1; human; telomerase RNA interactive protein-1; cancer; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW55887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW55887 standard;
                                             Human telomerase
                                                                   12-OCT-1998
                                                                                         AAW61347;
                                                                                                              AAW61347 standard;
                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                            cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAV25989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MITU ) MITSUBISHI CHEM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9807838-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detection; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JUL-1998
                                                                                                                                                                     205
                                                                                                                                                                                                              Local Similarity 47.
                                                                                                                                                                                         1 VPSYSFIRAHDSEVQDL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ر.
                                                                                                                                   6
                                                                                                                                                                   mpsyslslgeeeevedl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .1998-169149/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     telomerase;
                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ۲
                                                                                                                                                                                                                                                                                           development.
                                                                                                                                                                                                                                                                                                                                                                                                        Page 74-93; 106pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harada N,
                                                                                                                                                                                                                                                                     2625 AA;
                                                                                                                                                                                                                                                                                                                                                                                   sequence represents a human protein component of telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                   (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97JP-0031807.
96JP-0219761.
97JP-0018878.
                                                                                                                                                                                                                                                                                                       e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-JP02904
                                             RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein; 2625
                                                                                                              Protein;
                                                                  entry)
                                                                                                                                                                                                                                                                                                     cell growth or ageing and of the mechanisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                          44.28;
47.18;
                                            interactive protein-1 (TRIP1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ishikawa
                                                                                                                                                                       221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer; screening;
osis; cell growth; a
                                                                                                                2627
                                                                                                                                                                                                               Ψ
                                                                                                                                                                                                              Score 42; DB 19;
Pred. No. 1.8e+02;
3; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'n
                                                                                                                A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakamura
                                                                                                                                                                                                                                    DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ageing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inhibitor; elucidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ή,
                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                    Length 2625;
                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                              of
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RESULT
AAR99797
ID AARS
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AC AARS
AC AARS
DT 26-N
XX
DE Lys1
XX.
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                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                     SSSG
                                                                                                                                                                                                                                                                                                                                                                            This polypeptide comprises human telomerase RNA interactive protein-1 (TRIP1). Its amino acid sequence was deduced from CDNA clones (see AAV7865) obtained from a colon tumour cell line LIM1863 cDNA library. The invention relates to novel genes encoding components of the telomerase enzyme complex, including TRIP1 and telomerase protein 2 (TP2, see also AAW61349). These polypeptides may be useful as therapeutic agents in those cases where increasing TRIP1 activity or TP2 activity is desired, e.g. for treatment of HIV infection, AIDS and ageing disorders. In concert cells in which TRIP1 activity is to be decreased, such as in cancer cells in which TRIP1 activity and/or TP2 activity is to be decreased, such as in cancer cells in which TRIP1 activity and/or TP2 activity is to be decreased, such as in cancer cells in which TRIP1 activity and/or TP2 activity is to be decreased, such as in cancer cells in which TRIP1 activity and/or TP2 activity is to be decreased, such as in cancer cells in which TRIP1 activity and/or TP2 activity is to be decreased, such as in cancer cells in which TRIP1 activity and/or TP2 activity is to be decreased, such as in cancer cells in which TRIP1 activity and/or TP2 activity is to be decreased, such as in cancer cells in which TRIP1 activity and/or TP2 activity and to create antisense molecules, or DNA constructs may serve to disrupt or enhance TRIP1 and/or TP2 expression in cells, and to create dominant negative inhibitors of TRIP1 or TP2.
                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-1997;
15-NOV-1996;
11-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                 Lysine decarboxylase (W3110) of E.coli.
                                                 26-NOV-1996
                                                                                  AAR99797;
                                                                                                                   AAR99797 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Fig 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding human telomerase protein-2 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-297946/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harrington LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9821343-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune deficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regulating telomerase activity, e.g. for treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMGE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMGE-)
                                                                                                                                                                                                   205
                                                                                                                                                                                                                                 1 VPSYSFIRAHDSEVQDL 17
                                                                                                                                                                                                mpsys1s1geeeeved1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens
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AMGEN
                                                                                                                                                                                                                                                                   Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV27865
                                                                                                                                                                                                                                                                                                                                                    2627 AA;
                                                                                                                                                                                                                                                                   Conservative
                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CANADA INC
INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0951733.
96US-0871189.
97US-0873039.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Robinson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "residue 1155 is given as (translates as Gln)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150pp; English
                                                                                                                                                                                                                                                                                  44.28;
                                                                                                                                                                                                   221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                   713 AA
                                                                                                                                                                                                                                                                                 Score 42; DB 19;
Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                              Length 2627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xaa
                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transformant forms of Escherichia species (e.g. E.coli), in which the expression of the W3110 lysine decarboxylase gene (AAT34583), and, or the cadA gene (AAT34584), have been partly or wholly suppressed by deletion of part or all of the gene may be used for the efficient production of L-lysine when cultured.
                                                                                                                                                                                                                                                                                                                                                          allergy; metabolic diseacell cycle abnormality;
                                                                                                                                                                                                                                                                                                                                                             mitogen-activated protein kinase; MAP-kinase; graft-versus-host disease GVHD; Duchenne muscular dystrophy; therapy; cancer; autoimmune disease; allergy; metabolic disease; cell growth; cell proliferation; cytostatic cell cycle abnormality; cell differentiation; antiallergic; muscular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Production of L-lysine by culture of transformant which expression of new lysine decarboxylase gene has been partly or wholly suppressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 24-27; 45pp; Japanese.
                        (CEPT-) CEPTYR INC
                                                                         02-FEB-2000; 2000US-0179886
                                                                                                                            01-FEB-2001; 2001WO-US03429
                                                                                                                                                                                09-AUG-2001
                                                                                                                                                                                                                                   WO200157221-A2
                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; dual-specificity phosphatase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human dual-specificity phosphatase (DSP)-12 partial protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE06785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE06785 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AJIN ) AJINOMOTO CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-JUN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutant.
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                                                                                                                                                                                                                                                                                                                                     immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 lplyafinthstmdvsvqdm 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VPSYSFIRAH---DSEVQDL
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DB; AAT34583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41.5;
Pred. No. 47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            disease;
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RESULT
AAR40918
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell proliferation and cell cycle abnormalities. DSP is useful for identifying antibodies and other agents that inhibit DSP-12 and/or DSP-13 activity. DSP and the agents identified are useful for modulating cell proliferation, differentiation and survival. DSP is useful in screening assays for modulators of enzyme activity and substrate binding and for dephosphorylating a substrate of DSP-12 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated dual-specificity phosphatase polypeptide for treating cancer, graft-versus-host disease, autoimmune diseases, allergies, metabolic diseases, abnormal cell growth and abnormal cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR40918 standard; Protein;
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                                                                                                                                                              Inositol dehydrogenase gene - isolated from e.g. bacteria belonging to Bacillus subtilis, in large amt.
                                                                                                                                                                                                                                                                                                                                                                              30-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                 30-SEP-1991;
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e Bacillus subtilis inositol dehydrogenase gene has been cloned d sequenced. Microorganisms transformed by the coding sequence cultured to produce large amounts of recombinant inositol
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DB; AAQ48539.
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                                                                                                             Japanese
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dystrophy, cancer, graft-versus-host disease (GVHD), autoimmune di allergies, metabolic diseases, abnormal cell growth, abnormal cell proliferation and cell cycle abnormalities. DSP is useful for identifying antibodies and other agents that inhibit DSP-12 and/or

diseases

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RESULT :
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                                                      The present sequence is human dual-specificity phosphatase (DSP)-12 protein. Inactivation of mitogen-activated protein kinase (MAP-kinase) is mediated by dephosphorylation at a dual phosphorylation motif by DSP which is referred to as MAP-kinase phosphatase. An agent that modulates DSP is useful for treating a disorder selected from Duchenne muscular
                                                                                                                                                                   New isolated dual-specificity phosphatase polypeptide for treating cancer, graft-versus-host disease, autoimmune diseases, allergies, metabolic diseases, abnormal cell growth and abnormal cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; dual-specificity phosphatase; DSP-12; dual phosphorylation motif; mitogen-activated protein kinase; MAP-kinase; graft-versus-host disease; GVHD; Duchenne muscular dystrophy; therapy; cancer; autoimmune disease; allergy; metabolic disease; cell growth; cell proliferation; cytostatic; cell cycle abnormality; cell differentiation; antiallergic; muscular;
                                                                                                                                  Claim 1;
                                                                                                                                                                                                                                                             Luche RM,
                                                                                                                                                                                                                                                                                                            02-FEB-2000; 2000US-0179886
                                                                                                                                                                                                                                                                                                                                    01-FEB-2001; 2001WO-US03429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human dual-specificity phosphatase (DSP)-12 protein.
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nes 7; Conserv
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DB; AAD12965.
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                                                                                                                                 2; 81pp; English.
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386
                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Amino acid Thr is present at this location in the sequence shown in sequence listing of the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 249..269
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   The present sequence is human dual-specificity phosphatase (DSP)-12 mutant protein, C253S. Inactivation of mitogen-activated protein kinase (MAP-kinase) is mediated by dephosphorylation at a dual phosphorylation motif by DSP which is referred to as MAP-kinase phosphatase. An agent that modulates DSP is useful for treating a disorder selected from Duchenne muscular dystrophy, cancer, graft-versus-host disease (GVHD), autoimmune diseases, allergies, metabolic diseases, abnormal cell growth, abnormal cell proliferation and cell cycle abnormalities. DSP is useful for identifying antibodies and other agents that inhibit DSP-12 and/or DSP-13 activity. DSP and the agents identified are useful for modulating cell proliferation, differentiation and survival. DSP is
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                                                                                                                                                                                                                                       New isolated dual-specificity phosphatase polypeptide for treating cancer, graft-versus-host disease, autoimmune diseases, allergies, metabolic diseases, abnormal cell growth and abnormal cell
modulating
                                                                                                                                                                                                                          proliferation
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8; Conservative
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47.1%;
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07-APR-2000;
03-AUG-2000;
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Tateishi
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                                         amino acids, nucleic acids, vitamins, sa
particularly L-lysine. The present seque
in the exemplification of the invention
                                                               mutant of coryneform bactérium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids,
                                                                                                                    The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. Tare useful for identifying the mutation point of a gene derived from
                                                                                                                                                                                                expression
                                                                                                                                                                                                  Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium
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                     specification,
                                                                                                                                                                    Claim 17;
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          Patent
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                                                                                                                                                                    SEQ ID
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2000JP-0159162.
2000JP-0280988.
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                     but was obtained
           Office
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47.18;
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                                                                                                                                                                                                                                                                                    Ikeda
                     for this patent did not form obtained in electronic format
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da M, Ozaki A;
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Best Local
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28-DEC-1999;
25-JAN-2000;
31-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; SGP006 phosphatase polypeptide; phosphatase-related disease; immune-related disorder; ocular disease; organ transplant rejection; infection; diabetes; pain; sexual dysfunction; Alzheimer's disease; metabolic disorder; haematopoietic cancer; mood disorder; cardiant; parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; cardiovascular disease; brain; neuronal-associated disease; dyskinesia; attention disorder; cognition disorder; psychotic disorder; cytostatic; neurological disorder; virucide; nootropic; cerebroprotective; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neuroprotective; antibacterial; vulnerary; tranquilliser; antichypotensive; immunosuppressive; antipsoriatic; analgesic; hyperantifungal; dual specificity phosphatase; DSP; MAP kinase phosp MKP; migraine; chromosome 12q21.3-q22.
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          The present invention relates to phosphatase polypeptides, nucleotide sequences encoding them, as well as various products and methods useful for the diagnosis and treatment of various phosphatase-related diseases and conditions. Substance that modulates the activity of phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE04833;
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                                                                           Claim
                                                                                                  neuronal-associated diseases and
                                                                                                             Novel phosphatase polypeptide useful for treating cancers immune-related diseases and disorders, cardiovascular dise
                                                                                                                                                   N-PSDB;
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DB; AAD09491.
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99US-0175766.
2000US-0178078.
2000US-0179301.
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                                                                                                                                                                                                     Martinez
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Substance that used to treat
                                                                       186pp; English.
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                                                                                                    disease,
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Best Local S
Matches 8
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                                                                                                                                                                                                                                                                                                                                           03-SEP-1997;
20-JUN-1997;
22-JUL-1997;
        This sequence represents a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptic can be used in vaccines for eliciting protective antibodies to membe the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating a infection caused by a member of the Borrelia genus. The products car be used for detection of members of the Borrelia genus.
                                                                                                                            Claim 12;
                                                                                                                                                     products for the diagnosis, prevention and treatment caused by Borrelia, particularly Lyme disease
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                                                                                                                                                                                                                             WPI; 1999-189980/16.
                                                                                                                                                                                                                                                           Choi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Borrelia burgdorferi.
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12q21.3-q22.
                                                                                                                                                                                 New isolated Borrelia burgdorferi nucleic acids
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8; Conser
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97US-0050359.
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47.1%;
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Pred. No.
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Best Local
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N-PSDB; AAZ58277.
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                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                  Examples; Fig 1b; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              Infectious recombinant virus for use as insecticides or for expressing therapeutic proteins \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dall DJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heliothis armigera entomopoxvirus (HaEPV) DNA polymerase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CSIR ) COMMONWEALTH SCI & IND RES ORG.
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|||::||:|: |:
740 ysfnkkydsdvkslv 754
                                                                   684 pdysyilihdke 695
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                                                                                                2 PSYSFIRAHDSE 13
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                                                                                                                                         Score 41;
Pred. No.
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Pred. No.
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                                                                                                                            Mismatches
                                                                                                                                       DB 21; Length 1123; 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 20; Length 1120; 99;
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                                                                                                                          Gaps
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                                                                                                                            0;
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